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April 28, 2005, 15:52:12 ; Search time 2574 Seconds (without alignments) 9412.435 Million cell updates/sec
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Copyright (c) 1993 - 2005 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Description	119899 Cloning vec A95274 Sequence 5 AX212292 Sequence AR42712 Becherich 102541 Sequence 1 101971 Sequence 2 AR027070 Sequence 2 AR027070 Sequence 9 AR371194 Sequence 9 AR371194 Sequence 9 AR371194 Sequence 9 AR371194 Sequence 0 AR362785 Sequence 0 A7322 Cloning vec AX107930 Sequence AX107931 Sequence AX107931 Sequence AX107931 Sequence AX107931 Sequence AX107931 Sequence
SUMMARIES	SYNCVPTCF A95274 AX212292 AX212292 AX27127 1002541 101971 AR027070 101971 AR071194 BD008862 AR071194 BD008862 CVU47670 SYNNOMPA AX107930 CVU47322 AR362785 AR361211 AR370166
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/organism="synthetic construct"
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/mol_type="tunassigned DNA"
/db_xref="tuxon:32630"
/note="tuxon:32630"
/note="tuxon:32630"
Accession No. J01749 ( 3265-4350"
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Patent: WO 0159086-A 11 16-AUG-2001;
Sakata Seed Corporation (JP)
Location/Qualifiers
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Best Local Similarity 99.2%; Pred. No. 1.2e-134;
Matches 496; Conservative 0; Mismatches 0;
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Chaussee,A. and Zoolob,R.
ERAGENTS AND METHODS FOR DETECTING GENES RELATED TO MAJOR
HISTOCOMPATIBILITY COMPLEX OF DOMESTIC FOWL, SUCH AS CHICKEN
PATENT: WO 9927132-A 5 03-JUN-1999;
AGRONOMIQUE INST NAT RECH (FR); CHAUSSEE ANNE MARIE (FR)
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Best Local Similarity 100.0%; Pred. No. 1.5e-146;
Matches 500; Conservative 0; Mismatches 0; Indels 0;
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/db_xref="taxon:32644"
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Sequence 5 from Patent WO9927132.
A95274
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Gilbert, W., Broome, S.A., Villa-Komaroff, L.J. and Efstratiadis, A.A.
Recombinant DNA molecule
Patent: 10 4 565795-A 1 21-JAN-1986;
The President and Fellows of Harvard College; Cambridge, MA
Location/Qualifiers
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Pred. No. 1.2e-134;
0; Mismatches 0;
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Sequence 1 from Patent US 4565785.
102541 GI:268188
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/organism="unknown"
/mol_type="unassigned DNA"
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/db_xref="G1:16798370"
/db_xref="G1:16798370"
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IELDLANGKLILDSFPRERFPRLSTFKVLLCGAVLSRVDAGGEQLGRRIHYSQNDLVB
YSPVTEKHLTDGMTVRELCSAAVTMSDNTAANLLLTTIGGPKELTAFLHNMGDHVTRL
DRWEPELLNEALPDGMTVRELCSAAVTMSDNTAANLLLTTIGGPKELTAFLHNMGDHVTRL
DRSALPAGWFTADKSGAGERGSRGIIAALGPELTLASRQQLIDWMEADKNAGPL
ERGASLIKHW"
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BECharichia coli inhibitor-resistant beta-lactamase TEM-81
(blarem-81) gene, complete cds.
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(bases 1 to 1103)
Leflon-Guibout, V., Speldooren, V., Heym, B. and Nicolas-Chanoine, M. Epidemiological survey of amoxicillin-clavulanate resistance and corresponding molecular mechanisms in Escherichia coli isolates in France: new genetic features of bla (TEM) genes
Antimicrob. Agents Chemother. 44 (10), 2709-2714 (2000)
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Submitted (03-OCT-2001) Microbiology Service, Ambroise Pare
University Hospital, 9 avenue Charles de Gaulle, Boulogne 92100,
                                                                                                            GTCACGCTCGTCGTTTGGTATGGCTTCATTCAGCTCCGGTTCCCAACGATCAAGGCGAGT
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/transl_table=11
/product="inhibitor-resistant_beta-lactamase_TEM-81"
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Leflon-Guibout, V., Speldooren, V., Heym, B. and
Nicolas-Chanoine, M.-H.
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/mol type="genomic DNA"
/db_xref="taxon:562"
2097.1069
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/gene="blaTEM-81"
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Legoux, R., Maldonado, P. and Salome, M.
Method for the extraction of periplasmic proteins from prokaryotic microorganisms in the presence of arginine Patent: US 5856142-A 9 05-JAN-1999;
Location/Qualifiers
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/organism="unknown"
/mol_type="unassigned DNA"
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Sequence 9 from patent US 5856142.
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                                                                           301 AAGTAGTTCGCCAGTTAATAGTTTGCGCAACGTTGTTGCCATTGCTGCAGGCATCGTGGT
                                                                                      GTCACGCTCGTTTTGGTATGGCTTCATTCAGCTCCGGTTCCCAACGATCAAGGCGAGT
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Patent: US 4795699-A 2 03-JAN-1989;
President and Fellows of Harvard College; Cambridge, MA
Location/Qualifiers
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Sequence 2 from Patent US 4795699.
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/organism="unknown"
/mol_type="unassigned DNA"
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Tabor, S. and Richardson, C.C.
                                                                                                                                                                                                                       481 CAGAAGTAAGTTGGCCGCAG 500
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Best Local Similarity 99.2
Matches 496; Conservative
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Unclassified.
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Hepatitis C surrogate virus for testing the activity of Hepatitis C virus protease, a recombinant gene and a use thereof Hepatitis C surrogate virus for testing the activity of Hepatitis C surrogate virus for testing the activity of Hepatitis C brotease, a recombinant gene and a use thereof. BD008862 BD008862 GI:18637235 BD008862.1 GI:18637235 BD008862.1 GI:18637235 BD008862.1 GI:18637235 BD008862.1 GI:18637235
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1 (bases 1 to 2320)
Jangy S. K. and Halm, B. S.
Jangy S. K. and Halm, B. S.
Hepatitis C surrogate virus for testing the activity of Hepatitis C virus protease, a recombinant gene and a use thereof Patent: JP 2001503967-A 4 27-MAR-2001;
LG CHEMICALS CO LTD, OHANG UNIVERSITY OF SCIENCE AND TECHNOLOGY FOUNDATION
OS Artificial Sequence
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Jang, S.K. and Hahm, B.
Hepatitis C surrogate virus for testing the activity of hepatitis virus protease, a recombinant gene and a use thereof
Patent: US 6395471-A 13 28-MAY-2002,
Location/Qualifiers
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Pred. No. 1.3e-134;
0; Mismatches 0; Indels
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/wol_type="genomic DNA"
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Best Local Similarity 99.2%;
Matches 496; Conservative
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                                                            PAT 10-JUN-1998
                                                                                                                                                                                   Unknow...
Unclassified.
1 (bases 1 to 1905)
Legoux,R., Maldonado,P. and Salome,M.
Method for the extraction of periplasmic proteins from prokaryotic
Method for in the presence of arginine
Patent: US 5700665-A 9 23-DEC-1997;
Location/Qualifiers
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Sequence 13 from patent US 6395471.
AR371194 GI:34608123
                                                            186203 1905 bp
Sequence 9 from patent US 5700665.
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IB6203.1 GI:3205921
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Best Local Similarity 99.2
Matches 496; Conservative
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Location/Qualifiers
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92.4%; Score 462; DB 6; L
Best Local Similarity 99.2%; Pred. No. 1.3e-134;
Matches 496; Conservative 0; Mismatches 0;
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JP 2001503967-A/4
27-MAR-2001
25-JUN-1991 JP 1998504001
28-JUN-1996 KR 1996/24910
SUNG KEY JANG, BUN SUK HAHM
C12N15/51, C12Q1/70
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/organism="synthetic co
/mol_type="genomic DNA"
/db_xref="taxon:32630"
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/protein_id="CAA90506.1"
/db_xref="cd:938045"
/db_xref="cd:938045"
/translation="MRKKITGYTTVDISQWHRKEHFEAFQSVAQCTYNQTVQLDITAF
LKTVKKOKRKFYPAFIHILARLANNAHPEFRNAMKDGELVIWDSVHFCYTVFHEQTETF
SSLWSEYHDDFRQFHITYSQDVACYGENLAYFRGFERNFFYSANPWYSFTSFDLNV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                121 ACGATACGGGAGGGCTTACCATCTGGCCCCAGTGCTGCAATGATACCGCGAAGACCCCACG 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61 GCGATCTCTATTTCGTTCATCCCATAGTTGCCTGCAACTCCCCGTCGTGGATAACT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 ATATATGAGTAAAACTTGGTCTGACAGTTACCAATGCTTAATCAGTGAGGCACCTATCTCA
                                                                                                                                                                                                  Direct Submission
Submitted (19-JUL-1995) Rainer Haas, Infektionsbiologie,
Max-Planck-Institut fuer, Biologie, Spemannstr. 34, Tuebingen,
B.W., D-72076, Germany
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                        Improved ThWax mini-transposon system suitable for sequencing, shuttle mutagenesis and gene fusions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  note="rep-origin of bacteriophage fd (orifd)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 2408;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               complement(1554. .2342)
/product="mature beta-lactamase (BlaM)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               'note="M13 reverse primer (M13-RP1)"
                                                                                                                                                                                                                                                                                                                                                                                                                             1. 41
/ rpt Lype=INVERTED
complement (42. .59)
/note="M13.20 forward primer (M13-FP)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              .261. .1428
function="resolution site (res)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 462; DB 12;
Pred. No. 1.3e-134;
0; Mismatches 0;
                                                                                                                                                                                                                                                                                                          /organism="synthetic construct"
/mol_type="other DNA"
/db_xref="texon:32630"
/ldb_host="Escherichia coli K12"
1. 2408
/transposon="pTnMax9"
                                                                                                                                                                                                                                                                                                                                                                      coli K12"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   'note="gonococcal opa promoter"
.027. .1260
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   complement (77. .263)
/note="fd-terminator (tfd)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                complement (924. .1026)
/gene="catGC"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             complement (924. .1026)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        complement (264. .923)
shuttle mutagenesis and gene
Gene 167 (1-2), 53-57 (1995)
96144248
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2367. .2408
/rpt_type=INVERTED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             codon_start=1
transl_table=11
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                                                                                                                                                               3 (bases 1 to 2408)
Haas, R.
                                                                         (bases 1 to 2408)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 92.45
Best Local Similarity 99.25
Matches 496; Conservative
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                                                              8566811
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                                                                                             Haas, R.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         terminator
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SYN 06-JUL-2002

linear

DNA

2408 bp

ASTNMAX9

RESULT 11 ASTNWAX9

LOCUS DEFINITION ACCESSION VERSION KEYWORDS

synthetic construct
synthetic construct
other sequences;
artificial sequences.
1 (bases 1 to 2408)
Kahrs,A.F., Odenbreit,S., Schmitt,W., Heuermann,D., Meyer,T.F. and

An improved InMax mini-transposon system suitable for sequencing

наав, К

Z50143.1 GI:938044 beta-lactamase; chloramphenicol acetyltransferase; mini-transposon;

transposon.

ORGANISM

SOURCE

REFERENCE AUTHORS TITLE

Artificial DNA for pTnMax9 mini-transposon. Z50143

셤 õ a ò ద ઠે 셤 ઠે a ò g

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/db_xxeff="G1:1197853"
/fb_xxeff="G1:1197853"
/fb_xxeff="G1:1197853"
/fc_anslgt_ion="MSIQHERVALIPPFAAFCLPVFAHPETLVKVKDAEDQLGARVGY
/fc_anslgt_ion="MSIQHERVALIPFERVLLCGAVLSRVDAGOSQLGRRIHYSQNDLVB
/fc_anslgt_ion="MSIQHERVALIPFERVLLCGAVLSRVDAGOSQLGRRIHYSQNDLVB
/fc_anslgt_ion="MSIGHERVALIPFERVLLCGAVLSRVDGERITYRINMGDHVTRL
/fc_anslgt_ion="MSIGHERVALIPFERVLLCGAVLSRVQLIION"RADERVARGIA
/fc_anslgt_ion="MSIGHERVALIPFERVLLGELILASRQQLIION"RADERNRQIA
/fc_anslgt_ion="MSIGHERVALIPFERVLLGELILASRQQLIION"RADERNRQIA
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/fc_anslgt_ion="MSIGHERVALIPFERVLLGELILASRQIA"
/fc_anslgt_ion="MSIGHERVALIP
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A novel expression vector for high-level synthesis and secretion of
foreign proteins in Escherichia coli: overproduction of bovine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1808 Accaracceacecerraccarcrecececearcecerecearcaracece Adacceace 1866
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SYN 07-MAR-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                    1691 ATATATGAGTAAACTTGGTCTGACAGTTACCAATGCTTAATCAGTGAGGCACCTATCTCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1987 AAGTAGTTCGCCAGTTAATAGTTTGCGCAACGTTGTTGCCATTGCTGCAGGCATCGTGGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1751 GCGATCTGTCTATTTCGTTCAT-CCATAGTTGCCTG--ACTCCCCGTCGTGTAGATAACT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1927 TGGTCCTGCAACTTTATCCGCCTCCATCCAGTCTATTAATTGTTGCCGGGAAGCTAGAGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GTCACGCTCGTCGTTTGGTATGGCTTCATTCAGCTCCGGTTCCCAACGATCAAGGCGAGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TACATGATCCCCCCATGTTGTGCAAAAAGCGGTTAGCTCCTTCGGTCCTCCGATCGTTGT
                                                                                                                                                                                                                                                                                                                                                                                 1 ATATATGAGTAAACTTGGTCTGACAGTTACCAATGCTTAATCAGTGAGGCACCTATCTCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GCGATCTGTCTATTTCGTTCATCCCATAGTTGCCTGCAACTCCCCGTCGTGTAGATAACT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAGTAGTTCGCCAGTTAATAGTTTGCGCAACGTTGTTGCCATTGCTGCAGGCATCGTGGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2107 TACATGATCCCCCATGTTGTGCAAAAAAGCGGTTAGCTCCTTCGGTCCTCCGATGGTTGT
                                                                                                                                                                                                                                                                  Length 2783;
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                                                                                                                                                                                                                                                                                                                           Indels
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    2846
    organism="unidentified cloning vector"

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unidentified cloning vector
ther sequences; artificial sequences; vectors
1 (bases 1 to 2846)
                                                                                                                                                                                                                                                                     Score 462; DB 12;
Pred. No. 1.3e-134;
0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 source text: Cloning vector DNA, Location/Qualifiers
'protein_id="AAA88822.1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2846 bp
Cloning vector DNA, clone pTO-N.
M59367 M34008
M59367.1 GI:208909
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Gene 93 (2), 229-234 (1990)
91033032
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CAGAAGTAAGTTGGCCGCAG 2186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CAGAAGTAAGTTGGCCGCAG 500
                                                                                                                                                                                                                                                                        92.4%;
                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 99.2
Matches 496; Conservative
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SOURCE
ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LOCUS
DEFINITION
ACCESSION
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SYNNOMPA/c
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AUTHORS
TITLE
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MEDLINE
PUBMED
COMMENT
FEATURES
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/note="Portable expression cassette on Smal fragment; Smal
expression cassette may be inserted in a second vector"
                                  1701 CTCACCGGCTCCAGATTTATCAGCAATAAACCAGCCGGCGGAAGGGCCGAGCGCAGAAG 1760
                                                                                                                                                               1820
                                                                                                                                                                                                                                                                     1821 AAGTAGTTCGCCAGTTAATAGTTTGCGCAACGTTGTTGCCATTGCTGCAGGCATCGTGGT 1880
                                                                                                                                                                                                                                                                                                                                                                                 1881 GTCACGCTCGTCGTTTGGTATGGCTTCATTCAGCTCCCGGTTCCCAACGATCAGGCGAGT 1940
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CVU47670 2783 bp DNA circular SYN 20-FEB-1996 Cloning vector pJDC406, antisense expression vector for Escherichia
                                                                                                           300
                                                                                                                                                                                                                                                                                                                           420
                                                                                                                                                                                                                                                                                                                                                                                                                                       480
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                                                                                                                                                                                                                    360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          288. .297
/note="Antisense sequence may be inserted in unique XbaI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Inouye, M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  to regulate the
  TGGTCCTGCAACTTTATCCGCCTCCATCCAGTCTATTAATTGTTGCCGGGAAGCTAGAGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3 (bases 1 to 2783)
Coleman, J., Hirashima, A., Inokuchi, Y., Green, P.J. and Inouye, M.
Direct Submission
                                                                                                                                             GTCACGCTCGTTTTGGTATGGCTTCATTCAGCTCCGGTTCCCAACGATCAAGGCGAGT
                                                                                                                                                                                                                                                                                                                                                                                                                                       421 TACATGATCCCCCATGTTGTGCAAAAAGCGGTTAGCTCCTTCGGTCCTCCGATCGTTGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2 (bases 1 to 2783)
Coleman, J., Hirashima, A., Inokuchi, Y., Green, P.J. and A novel immune system against bacteriophage infection complementary RNA (micRNA)
Nature 315 (6020), 601-603 (1985)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /organism="Cloning vector pJDC406"
/mol type="genomic DNA"
/mol type="genomic DNA"
/db xref="taxon:4562"
/noTe="antisense RNA expression vector"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     mRNAB
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Cloning vector pJDC406
Cloning vector pJDC406
1 (basequences; artificial sequences; vectors.)
Coleman,J., Green,P.J. and Inouye,M.
The use of RNMs complementary to specific mRNMs expression of individual bacterial genes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /product="beta-lactamase"
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complement(1717. .2577)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2001 CAGAAGTAAGTTGGCCGCAG 2020
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CAGAAGTAAGTTGGCCGCAG 500
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/transl_table=11
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U47670
U47670.1 GI:1197852
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1926

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1986

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1807

9

Gaps

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2046

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Query Match
Best Local Similarity 99.2%;
Matches 496; Conservative
92.4%;
Query Match 92.4
Best Local Similarity 99.2
Matches 496; Conservative
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                                                                                                                                        Gaps
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                                                                                                            Length 2846;
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/organism="synthetic construct"
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                                                                                                             Score 462; DB 12;
Pred. No. 1.3e-134;
0; Mismatches 0;
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                                        21. .39
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81. .143
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Best Local Similarity 99.2%;
Matches 496; Conservative
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1 (bases 1 to 2913)

Edman, J.C., Clauser, E. and Ellis, L.

Direct Submission
Submitted (26-JAN-1996) J. C. Edman, Hormone Research Institute,
University of California, San Francisco, Box 0534, San Francisco,
CA 94143-0534, USA

Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 ATATATGAGTAAACTTGGTCTGACAGTTACCAATGCTTAATCAGTGAGGCACCTATCTCA
                               Gaps
                                                                                  1903 AAGTAGTTCGCCAGTTAATAGTTTGCGCAACGTTGTTGCCATTGCTGCAGGCATCGTGGT
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/organism="unidentified cloning vector"
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Pred. No. 1.3e-134;
0; Mismatches 0;
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 Score 462; DB 6; I
Pred. No. 1.3e-134;
0; Mismatches 0;
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C10ning vector DNA, complete sequence.
U47322
U47322.1 GI:1197727
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Search completed: April 29, 2005, 04:24:22 Job time : 2579 secs

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Run on:

April 28, 2005, 18:49:09 ; Search time 425 Seconds (without alignments) 6964.402 Million cell updates/sec

US-10-043-160-5_COPY_1_500 500 Title: Perfect score:

1 atatatgagtaaacttggtc......sagaagtaagttggccgcag 500 Sequence:

IDENTITY_NUC Gapop 10.0 , Gapext 1.0 Scoring table:

4390206 segs, 2959870667 residues Searched:

8780412

seq length: 0 seq length: 200000000 0B 0B Minimum Maximum

Total number of hits satisfying chosen parameters:

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Geneseq 16Dec04:* Database

geneseqn2004as:* geneseqn2004bs:* geneseqn2003cs:* geneseqn2003ds:* geneseqn2003as:* geneseqn2002bs:* geneseqn2001bs:* geneseqn2002as:* geneseqn2003bs:* genesegn1980s:* genesegn1990s:* geneseqn2001as: 9

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

ss Coding Nucleotid Aax60263 Nucleic a DNA seque Human imm Human imm Human imm Genomic s Genomic B Genomic Genomic Description Aa841782 G Aa841875 G Aak85505 H Aak85205 H Aak8455 H Aal02889 H Aal02919 H Aa827796 L Aak69615 B Aak85438 B Aak85488 B Aan91727 B Aaa14722 B Aas11826 C Aas41766 Aas41810 Aas41859 AAK69615 AAK85438 AAK85488 AAX60263 AAS41826 ü DB Query Match Length 2212 2212 Score Result Š

Aas41818 Genomic s	Aas41867 Genomic s	Aas41776 Genomic s	Aak85447 Human imm	Aak69622 Human imm	Aak69623 Human imm	Aak85446 Human imm	Aak85496 Human imm	Aak85497 Human imm	Aal02882 Human rep	Human	Human	Aal02914 Human rep	Adb94599 Novel hum	Adb94605 Novel hum	Aag11202 Plasmid p	Aaq46606 Plasmid p		Aaf83095 Nucleotid	Aag05745 Plasmid P	Aaf83096 Nucleotid	Aav12724 Plasmid p		Aaz22063 Nucleotid	Abk11528 Human-der
AAS41818	AAS41867	AAS41776	AAK85447	AAK69622	AAK69623	AAK85446	AAK85496	AAK85497	AAL02882	AAL02884	AAL02912	AAL02914	ADB94599	ADB94605	AAQ11202	AAQ46606	AAA14802	AAF83095	AAQ05745	AAF83096	AAV12724	AAV39219	AAZ22063	ABK11528
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2213	2213	2213	2213	2213	2213	2213	2213	2213	2213	2213	2213	2213	2213	2213	2522	2583	2731	2870	3003	3097	3122	3122	3122	3158
92.4	92.4	92.4	92.4	92.4	92.4	92.4	92.4	92.4	92.4	92.4	92.4	92.4	92.4	92.4	92.4	92.4	92.4	92.4	92.4	92.4	92.4	92.4	92.4	92.4
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c 21	c 55	c 23	c 24	c 25	c 26	c 27	c 28	c 29	c 30	c 31	c 32	c 33	c 34	c 35	c 36	c 37	38	39	40	41	42	43	44	45

ALIGNMENTS

RESULT 1

BP

AAX60263 standard; DNA; 43226

AAX60263;

(first entry)

12-AUG-1999

Nucleic acid sequence from C121 gene of system B of chicken MHC.

Resistance; tumour development; Marek disease tumour; chicken; system B; system Rfp-Y; poultry major histocompatibility complex; MHC; class II B-L gene; gene 17.5; gene 12.3; gene B-FIV; class I; genotype; selection; breeding; virus-induced tumour; C121 gene; ss.

Gallus sp.

FR2771422-A1

28-MAY-1999

97FR-00014669. 21-NOV-1997; 97FR-00014669. 21-NOV-1997; CNRS) CNRS CENT NAT RECH SCI

WPI; 1999-329699/28

Chicken nucleic acid involved in controlling tumor susceptibility.

Claim 2; Fig 5; 49pp; French

The specification describes nucleic acid sequences from genes (or related regions) that encode proteins involved in controlling resistance or susceptibility to development of tumours (e.g., marek disease tumours) in chickens. The nucleic acid sequences include sequences from gene of systems B or Rfp-Y of the poultry major histocompatibility complex (MHC), other than genes of class II B-L and genes 17.5, 12.3 or B-FIV of class I. The nucleic acid sequences are used to genotype poultry, particularly to select (for breeding) birds resistant to virus-induced tumours. The present sequence represents a nucleic acid sequence from a gene of system

DNA encod DNA encod

AAS27796 AAS27802

Genomic B Human imm Human imm Human imm Human rep Human rep

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                 Sequence 43226 BP; 10365 A; 10522 C; 11244 G; 10981 T; 0 U; 114 Other;
                                                                                                                                               GCGATCTGTCTATTTCGTTCATCCCATAGTTGCCTGCAACTCCCCGTCGTGTAGATAACT
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                                                                                             1 ATATATGAGTAAACTTGGTCTGACAGTTACCAATGCTTAATCAGTGAGGCACCTATCTCA
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                                                                       Gaps
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                                          Length 43226;
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                                                                   Indels
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recombinase recognition site; ampicillin resistance; ds.
                                        ; Score 500; DB 2; I; Pred. No. 8.4e-122; 0; Mismatches 0;
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Matches 500; Conservative 0
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The invention relates to a method of preparing a transformed plant that comprises introducing into plant cells, a construct of at least one agrobacterium oncogene (II), whose expression enables the transformed cells (TC) to grow under conditions insufficient for the growth of untransformed cells, selecting TC, negating the effect of (II) in TC and regenerating morphologically normal transformed plants from TC. The DNA vector of the invention comprises in 5'-3' direction, a DNA sequence homologous to a left portion of the right or left border region of the T-DNA region of a Ti-plasmid, a recombinase recognition site (RRS), and a region of DNA homologous to a right portion of the right or left border region of the T-DNA region of a Ti-plasmid; and is selected from pRBC-1, pLBC-1 or pLBC-2. The method is useful for producing transformed plants;
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Producing transformed plant, involves transforming plant cells with Agrobacterium oncogene-construct, selecting transformed cells, negating oncogene effect and regenerating morphologically normal transformed
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Pred. No. 6.2e-112;
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     Human; oxidoreductase enzyme; transferase; hydrolase; lyase; isomerase;
                                                                        ligase; hyperproliferative disorder; immunodeficiency disorder; autoimmune disorder; neurological disorder; metabolic disorder; inflammatory disorder; cardiovascular disorder; reproductive disorder; blood-related disorder; infectious disorder; anti arthritic; nephrotropic; anticoagulant; ds.
                   sequence #82 encoding novel human enzyme polypeptide
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2000US-0215135P-
2000US-0216647P-
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16-MAR-2000;
17-MAR-2000;
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19-MAY-2000;
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Human; oxidoreductase enzyme; transferase; hydrolase; isomerase; ligase; hyperproliferative disorder; immunodeficiency disorder; autoimmune disorder; neurological disorder; metabolic disorder; inflammatory disorder; cardiovascula disorder; reproductive disorder; blood-related disorder; infectious disorder; gene therapy; cytostatic; anti arthritic; nephrotropic; anticoagulant; ds.
                                     TACATGATCCCCCATGTTGTGCAAAAAAGCGGTTAGCTCCTTCGGTCCTCCGATCGTTGT
                                                                                                                                                                                                                                                                                                                                                                   Genomic sequence #126 encoding novel human enzyme polypeptide.
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                                                                                                                                                                                                                                                                                                                                                                                                      Disclosure; SEQ ID NO 1892; 1180pp; English.
                                                                                                                                                                                                                                     Ruben SM
06-DEC-2000; 2000US-0251479P.
08-DEC-2000; 2000US-0251856P.
08-DEC-2000; 2000US-0251868P.
08-DEC-2000; 2000US-0251869P.
08-DEC-2000; 2000US-0251989P.
11-DEC-2000; 2000US-0251990P.
05-JAN-2001; 2000US-0251990P.
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The present invention relates to the isolation of novel human enzyme polypeptides (AAU22915-AAU3814), and the CDNA and genomic sequences encoding them. The enzyme polypeptides of the invention may comprise the functional classes of oxidoreductases, transferases, hydrolases, lyases, isomerases or ligases. The sequences of the invention are useful in the disorders including hyperproliferative disorders (e.g. cancer), immunodeficiency disorders (e.g. ALDS) autoimmune disorders (e.g. arthritis), neurological disorders (e.g. ALDS) autoimmune disorders (e.g. arthritis), neurological disorders (e.g. ALDS) autoimmune disorders (e.g. arthritis), neurological disorders (e.g. ALDS) autoimmune disorders (e.g. arthritis), inflammatory disorders (e.g. asthma), cardiovascular disorders (e.g. atherosclerosis), blood-related disorders (e.g. lasemophila), reproductive disorders (e.g. influenca). Inflammatory disorders (e.g. asthma) infectious disorders (e.g. Influenca). The polymuclectides of the invention can also be used in gene therapy. AAS41685-AAS42192 represent C. DNA sequences encoding for the novel human enzyme polypeptides of the invention. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.Wipo.int/Published_pct_sequences
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Pred. No. 6.6e-112;
0; Mismatches 0; Indels 4
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                   2000US-0249215P.
2000US-0249216P.
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2000US-0249265P.
2000US-0249265P.
2000US-0249269P.
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Matches 496; Conservative
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978 ACGATACGGGAGGGCTTACCATCTGGCCCCAGTGCTGCAATGATACCGCG-AGACCCACG 920
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                         241 TGGTCCTGCAACTTTATCCGCCTCCATCTATTAATTGTTGCCGGGAAGCTAGAGT
                                                     AAGTAGTTCGCCAGTTAATAGTTTGCGCAACGTTGTTGCCATTGCTGCAGGCATCGTGGT
                                                                                                   GTCACGCTCGTCGTTTGGTATGGCTTCAGCTCCGGTTCCCAACGATCAAGGCGAGT
                                                                                                           421 TACATGATCCCCCATGTTGTGCAAAAAGCGGTTAGCTCCTTCGGTCCTCCGATCGTTGT
                                                                                                                                       Genomic sequence #175 encoding novel human enzyme polypeptide.
                                                                                                                                                            CAGAAGTAAGTTGGCCGCAG 500
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The present invention relates to the isolation of novel human enzyme polypeptides (AAU22915-AAU23814), and the CDNA and genomic sequences encoding them. The enzyme polypeptides of the invention may comprise the functional classes of oxidoreductases, transferases, hydrolases, lyases, isomerases or ligases. The sequences of the invention are useful in the disorders including hyperproliferative disorders (e.g. cancer), immunodeficiency disorders (e.g. AIDS) autoimmune disorders (e.g. cancer), immunodeficiency disorders (e.g. AIDS) autoimmune disorders (e.g. arthritis), neurological disorders (e.g. AIDS) autoimmune disorders (e.g. arthritis), neurological disorders (e.g. AIDS) autoimmune disorders (e.g. phenylketonuria), inflammatory disorders (e.g. asthma), cardiovascular disorders (e.g. atherosclerosis), blood-related disorders (e.g. phenylketonuria), inflammatory disorders (e.g. asthma), cardiovascular disorders (e.g. influence). The polymucleotides of the infectious disorders (e.g. Influence). The polymucleotides of the invention can also be used in gene therapy. AAS41685-AAS42192 represent invention. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from MIPO at ftp. wipo.int/pub/published_pct_sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Novel polypeptides and polynucleotides useful for diagnosing, preventing,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Disclosure; SEQ ID NO 1985; 1180pp; English.
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                                                                                                                                              4
                                                                 Score 462; DB 4; Length 2022;
Pred. No. 6.6e-112;
0; Mismatches 0; Indels
Sequence 2022 BP; 513 A; 478 C; 512 G; 518 T; 0 U; 1 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     481 CAGAAGTAAGTTGGCCGCAG 500
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02-MAR-2000; 2000US-0186550P.
16-MAR-2000; 2000US-0189874P.
17-MAR-2000; 2000US-0190076P.
18-ARK-2000; 2000US-0198123P.
19-MAY-2000; 2000US-025515P.
                                                                 Query Match
Best Local Similarity 99.2%;
Matches 496; Conservative
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04-FEB-2000;
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FR 07-JUN-2000; 2000US-0219467P.
FR 30-JUN-2000; 2000US-0211135P.
FR 70-JUN-2000; 2000US-0211135P.
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FR 11-JUC-2000; 2000US-023334FP.
FR 11-JUC-2000; 2000US-023334FP.
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AAKS4951 to AAK64702 encode the human immune/haematopoietic antigen (I) amino acid sequences given in AAM82170 to AAM91921. (I) have cytostatic activity, and can be used in gene therapy and vaccine production. (I) proteins and polynuclectides may be used in the prevention, diagnosis and treatment of diseases associated with inappropriate (I) expression. For example, they may be used to treat disorders associated with decreased
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Nucleic acids encoding human immune/hematopoietic antigen polypeptides, useful for preventing, diagnosing and/or treating cancers and metastasis.
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                      2000US-0241787P

2000US-0241808P

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2000US-0244617P

2000US-0246474P

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2000US-0249245P
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2000US-0249300P
2000US-0250160P
2000US-0250160P
2000US-0250160P
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2000US-0256719P
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20-0CT-2000;
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01-NOV-2000;
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05-SEP-2000;
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22-AUG-2000;
23-AUG-2000;
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             expression by rectifying mutations or deletions in a patient's genome that affect the activity of (1) by expressing inactive proteins or to supplement the patients own production of (1). Additionally, (1) polynucleotides may be used to produce the secreted (1), by inserting the nucleic acids into a host cell and culturing the cell to express the protein. (1) proteins and polynucleotides may be used to prevent, adjagnose and treat immune/haematopoietic-related diseases, especially cancers and cancer metastases of haematopoietic-derived cells. AAK64703 to AAK87594 represent human immune/hematopoietic antigen genomic sequences from the present invention. AAK54992 to AAK54950 and AAM3169 represent sequences used in the exemplification of the present invention
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cytostatic; gene therapy; vaccine; metastasis; ds.
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Best Local Similarity 99.2%; Pred. No. 6.6e-112;
Matches 496; Conservative 0; Mismatches 0;
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Nucleic acids encoding human immune/hematopoietic antigen polypeptides, useful for preventing, diagnosing and/or treating cancers and metastasis.

Disclosure; SEQ ID NO 40250; 3071pp + Sequence Listing; English.

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2000US-0249211P.
2000US-0249212P.
2000US-0249214P.
2000US-0249215P.
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AAKS4951 to AAK64702 encode the human immune/haematopoietic antigen (I)
amino acid sequences given in AAM82170 to AAM91921. (I) have cytostatic
activity, and can be used in gene therapy and vaccine production. (I)
activity, and can be used in gene therapy and vaccine production. (II)
consistent of diseases associated with inappropriate (I) expression. For
example, they may be used to treat disorders associated with decreased
consistent affect the activity of (I) by expressing inactive proteins or to
that affect the activity of (I) by expressing inactive proteins or to
consplement the patients own production of (I). Additionally, (I)
conjournelectides may be used to produce the secreted (I), by inserting the
concern acids into a host cell and culturing the cell to express the
concerns and cancer metastesses of haematopoietic-related diseases, especially
cancers and cancer metastesses of haematopoietic-derived cells. AAK64703
connects and cancer metastesses of haematopoietic-derived cells. AAK64703
connects from the present invention. AAK54942 to AAK845950 and AAM82169
crepresent sequences used in the exemplification of the present invention
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Ruben SM;

Rosen CA, Barash SC, WPI; 2001-483426/52.

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2000US - 0239335P
2000US - 0239933F
2000US - 0240960P
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   Human; immune; haematopoietic; immune/haematopoietic antigen; cancer; cytostatic; gene therapy; vaccine; metastasis; ds.
               Human immune/haematopoietic antigen genomic sequence SEQ ID NO:40300
                                                                                                                                                                                 17-JAN-2001; 2001WO-US001354
                                                                                                                      WO200157182-A2
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06-SEP-2000;
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01-SEP-2000;
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                                                                                           Ното варіепв
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04-FEB-2000;
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770 Accaraccededesecritaccarcresececearicaresearcaraccese-Acaecearca
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sandwich hybridisation assays use label probes which are complementary to portions of the CDS (tag a) and capture probes which are complementary to portions which are downstream of the CDS. (Updated on 25-WAR-2003 to correct PR field.) (Updated on 25-WAR-2003 to correct PA field.)
                                                                                                                                                                                                                                                                                                           Neisseria gonorrhoeae plasmid; beta-Lactamase TEM-1 gene; capture probe;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Nucleic acid multimer for hybridisation assays - having single-stranded oligo-nucleotide units capable of binding specifically to sequences of
                                                                                                                                                                                                                                                  ss Coding strand of a portion of a 7.3 kb Neisseria gonorrhoeae plasmid carrying the beta-Lactamase TEM-1 gene.
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92.4%; Score 462; DB 1; Length 2039;
Best Local Similarity 99.2%; Pred. No. 6.6e-112;
Matches 496; Conservative 0; Mismatches 0; Indels
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619 CAGAAGTAAGTTGGCCGCAG 600
                                                                                                                  ВР
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88US-00185201.
88US-00252638.
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                                                                                                                  AAN91727 standard; DNA; 2039
                                                                                                                                                                                               (revised)
(first entry)
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30-SEP-1988;
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13-APR-1990
                                                                                                                                                                                                                                                                                                                                      label probe.
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                                                                                                                                                                                                                                                                                                           AAK54951 to AAK64702 encode the human immune/haematopoietic antigen (I)
amino acid sequences given in AAM82170 to AAM91921. (I) have cytostatic
activity, and can be used in gene therapy and vaccine production. (I)
proteins and polymucleotides may be used in the prevention, diagnosis and
treatment of diseases associated with inappropriate (I) expression. For
expression by rectifying mutations or deletions in a patient's genome
cample, they may be used to treat disorders associated with decreased
expression by rectifying mutations or deletions in a patient's genome
that affect the activity of (I) by expressing inactive proteins or to
supplement the patients own production of (I). Additionally, (I)
c supplement the patients own production of (I). Additionally, (I)
protein a host cell and culturing the cell to express the
protein. (I) proteins and polymucleotides may be used to prevent,
diagnose and treat immune/haematopoietic-derived cells. AAK64703
to AAK87694 represent human immune/haematopoietic antigen genomic
sequences from the present invention. AAK54942 to AAK54950 and AAM82169
crepresent sequences used in the exemplification of the present invention
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                                                                                                                                                                                                                     Nucleic acids encoding human immune/hematopoietic antigen polypeptides, useful for preventing, diagnosing and/or treating cancers and metastasis.
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                                                                                                                                                                                                                                                                               Disclosure; SEQ ID NO 40300; 3071pp + Sequence Listing; English
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Pred. No. 6.6e-112;
0; Mismatches 0; Indels
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                                                                                                                                                Ruben SM
                          08-DEC-2000; 2000US-0251990P.
11-DEC-2000; 2000US-0254097P.
05-JAN-2001; 2001US-0259678P.
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Best Local Similarity 99.2%;
Matches 496; Conservative
          08-DEC-2000; 2000US-0251989P
                                                                                                         (HUMA-) HUMAN GENOME SCI INC.
                                                                                                                                              Barash SC,
                                                                                                                                                                                   WPI; 2001-483426/52
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Treating cancer using viral vectors which encode enzymes that convert inactive drugs to active cytotoxic agents, expression of the enzyme is tissue specific therefore targeting the effects of the drug to tumor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Cellular cytotoxicity; tumor cell; expression vector; beta-lactamase; replication-deficient adenovirus type 5; suicide gene therapy; cancer cell; chemotherapy; beta-lactamase prodrug enzyme; prodrug anticancer; tumor; leukemia; breast cancer; Wilm's tumor; small cell lung carcinoma; Ewing's sarcoma; colon carcinoma;
                                                                                         301 AAGTAGTTCGCCAGTTAATAGTTTGCGCAACGTTGTTGCCATTGCTGCAGGCATCGTGGT
                                                                                                                                                                                                                                                  GTCACGCTCGTCGTTTGGTATGGCTTCATTCAGCTCCGGTTCCCAACGATCAAGGCGAGT
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                                                                    TGGTCCTGCAACTTTATCCGCCTCCATCCAGTCTATTAATTGTTGCCGGGAAGCTAGAGT
                                                                                                                                                                                     GTCACGCTCGTCGTTTGGTATGGCTTCATTCAGCTCCGGTTCCCAACGATCAAGGCGAGT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Nucleotide sequence of region A of vector Ad5RSVbeta-lactamase.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Rous sarcoma virus.
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08-AUG-2000
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LD AAA14722/c
LD AAA14
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adenovirus genome has a deletion in an B1 and/or E3 region, and the betacolactamase sequence is inserted within this region. The vectors are used for suicide gene therapy. This involves introducing genes into cancer cells that encode enzymes capable of converting inactive drugs into active cancer killing agents. If tissue specific promoters are coupled to the prodrug enzymes, then production of the prodrug will be tissue specific and targeted to the tumor. Therefore the cancer cells act as specific and targeted to the tumor. Therefore the cancer cells act as their own factories to activate chemotherapy agents and commit suicide. Beta-lactamase prodrug enzymes convert prodrug TCM into an active anticanner agent which is cytotoxic to cancer cells PPC-1. The method is used to treat patients with cancers of the brain, bladder or prostate. It may also be used to treat a range of other tumors such as leukemia, breast cancer, will's tumor, small cell lung carcinoma, Ewing's sarcoma, colon carcinoma and papillary adenocarcinomas. The present sequence represents region A of vector AdSRSVbeta-lactamase, a vector of the invention. (Updated on 06-AUG-2003 to correct OS field.)
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ligase; hyperproliferative disorder; immunodeficiency disorder;
autoimmune disorder; neurological disorder; metabolic disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1993 ATATATGAGTAAACTTGGTCTGACAGTTACCAATGCTTAATCAGTGAGGCACCTATCCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1757 TGGTCCTGCAACTTTATCCGCCTCCATCCAGTCTATTAATTGTTGCCGGAAGCTAGAGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         121 ACGATACGGGAGGGCTTACCATCTGGCCCCAGTGCTGCAATGATACCGCGAAGACCCACG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     361 GTCACGCTCGTTTGGTATGGCTTCATTCAGCTCCGGTTCCCAACGATCAAGGCGAGT
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Pred. No. 6.6e-112;
0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 2187 BP; 562 A; 477 C; 592 G; 556 T; 0 U; 0 Other;
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Best Local Similarity 99.2°
Matches 496; Conservative
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2000US-0234998P
2000US-0235484P
2000US-0235834P.
2000US-0236337P.
2000US-0236367P.
2000US-0236367P.
2000US-0236367P.
2000US-0236368P.
2000US-023638P.
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2000US-0239937P.
2000US-0240960P.
2000US-024121P.
2000US-0241785P.
2000US-0241786P.
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2000US-0241808P-
2000US-0241808P-
2000US-0246474P-
2000US-0246474P-
2000US-0246477P-
2000US-0246477P-
2000US-0246477P-
2000US-0246524P-
2000US-0246532P-
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2000US-0249265P.
2000US-0249297P.
2000US-0249299P.
2000US-0249300P.
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2000US-0251988P
2000US-0256719P
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2000US-0251990P
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              21-SEP-2000;
25-SEP-2000;
25-SEP-2000;
26-SEP-2000;
27-SEP-2000;
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29-SEP-2000;
29-SEP-2000;
29-SEP-2000;
29-SEP-2000;
29-SEP-2000;
02-OCT-2000;
02-OCT-2000;
13-OCT-2000;
20-OCT-2000;
20-OC
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01-DEC-2000;
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17-NOV-2000;
17-NOV-2000;
17-NOV-2000;
                inflammatory disorder; cardiovascular disorder; reproductive disorder; blood-related disorder; infectious disorder; gene therapy; cytostatic; anti arthritic; nephrotropic; anticoagulant; ds.
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2000US-018652BP.
2000US-0184564P.
2000US-0189874P.
2000US-0198123P.
2000US-029467P.
2000US-0209467P.
2000US-0214886P.
2000US-0215135P.
2000US-0215135P.
2000US-0215135P.
2000US-0215135P.
2000US-021481P.
2000US-021513P.
2000US-0218419P.
2000US-0225266P.
2000US-0225266P.
2000US-0225266P.
2000US-0225266P.
2000US-0225214P.
2000US-0225214P.
2000US-022526P.
2000US-0225218P.
2000US-0225718P.
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2000US-0229513P.
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2000US-0230438P.
2000US-0231242P.
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2000US-0231413P.
2000US-0231414P.
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2000US-0232081P.
2000US-0231968P.
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2000US-0234223P
                                                                                                                            WO200155301-A2
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24-FEB-2000;

16-MAR-2000;

16-MAR-2000;

19-MAY-2000;

19-MAY-2000;

10-JUL-2000;

28-JUL-2000;

11-JUL-2000;

11-JUL-2000;

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11-JUL-2000;

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11-AUG-2000;

14-AUG-2000;

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22-AUG-2000;
22-AUG-2000;
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30-AUG-2000;
01-SEP-2000;
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05-SEP-2000;
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08-SEP-2000;
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14-AUG-2000;
18-AUG-2000;
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                                                                                           Homo sapiens
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21-SEP-2000;
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* $\frac{1}{2}$ $\frac{1}{2}$
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RESULT 12
                                                                 AAS41782,
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                                                                                                                                                                                         The present invention relates to the isolation of novel human enzyme polypeptides (AAU22915-AAU23814), and the CDNA and genomic sequences encoding them. The enzyme polypeptides of the invention may comprise the functional classes of exidereductases, transferases, hydrolases, lyases, isomerases or ligases. The sequences of the invention are useful in the clasmests, prevention and/or prognosis of a wide range of disgnosis, treatment, prevention and/or prognosis of a wide range of clasmosis, treatment, prevention and/or prognosis of a wide range of immunodeficiency disorders (e.g. Alzheimer's disorders (e.g. arthritis), neurological disorders (e.g. Alzheimer's disorders (e.g. atthma), cardiovascular disorders (e.g. atherosclerosis), blood-related disorders (e.g. heemophilia), reproductive disorders (e.g. infertility) and infectious disorders (e.g. Influenza). The polymucleotides of the invention can also be used in gene therapy. AAS41685-AAS42192 represent DNA sequences encoding for the novel human enzyme polypeptides of the invention. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
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                                                                                                               Novel polypeptides and polynucleotides useful for diagnosing, preventing, treating neural, immune system, muscular, reproductive, pulmonary, cardiovascular, renal, proliferative disorders and cancerous diseases.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TGGTCCTGCAACTTTATCCGCCTCCATCCAGTCTATTAATTGTTGCCGGGAAGCTAGAGT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 2212;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 462; DB 4; L
Pred. No. 6.6e-112;
0; Mismatches 0;
                                                                                                                                                                   Disclosure; SEQ ID NO 1952; 1180pp; English
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                                                               Ruben SM;
11-DEC-2000; 2000US-0254097P.
05-JAN-2001; 2001US-0259678P.
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                                      (HUMA-) HUMAN GENOME SCI INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity 99.2
nes 496; Conservative
                                                               Barash SC,
                                                                                        WPI; 2001-465566/50
                                                               Rosen CA,
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Human, oxidoreductase enzyme, transferase; hydrolase; lyase; isomerase; ligase; hyperproliferative disorder; immunodeficiency disorder; autoimmune disorder; neurological disorder; metabolic disorder; inflammatory disorder; cardiovascular disorder; reproductive disorder; blood-related disorder; infectious disorder; gene therapy; cytostatic; anti arthritic; nephrotropic; anticoagulant; ds.
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The present invention relates to the isolation of novel human enzyme polypeptides (AAU22915-AAU23814), and the cDNA and genomic sequences concoling them. The enzyme polypeptides of the invention may comprise the functional classes of exidoreductases, transferases, hydrolases, lyases, isomerases or ligases. The sequences of the invention are useful in the diagnosis, transferation and/or prognosis of a wide range of clasporders including hyperproliferative disorders (e.g. cancer), immunodeficiency disorders (e.g. AIDS) autoimmune disorders (e.g. atthrish), neurological disorders (e.g. Alzheimer's disease), metabolic disorders (e.g. phemylketonuria), inflammatory disorders (e.g. atthma), cardiovascular disorders (e.g. atherosclerosis), blood-related disorders (e.g. phemylketonuria), inflammatory disorders (e.g. atthma), cardiovascular disorders (e.g. atherosclerosis), blood-related disorders (e.g. infectious disorders (e.g. Influenza). The polymucleotides of the invention can also be used in gene therapy. AAA31685-AAA3192 represent invention and so be used in gene therapy. AAA31685-AAA3192 represent invention. Note: The sequence data for this patent dinot form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
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17-NOV-2000; 2000US-0249245P.
17-NOV-2000; 2000US-0249264P.
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17-NOV-2000; 2000US-0249300P.
01-DEC-2000; 2000US-0250160P.
01-DEC-2000; 2000US-0250130P.
05-DEC-2000; 2000US-0251930P.
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                                   TACATGATCCCCCATGTTGTGCAAAAAAGCGGTTAGCTCCTTCGGTCCTCCGATCGTTGT
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17-MAR-2000;
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05-JAN-2001; 2001US-0259678P
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Best Local Similarity 99.2%;
Matches 496; Conservative
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                                              17-NOV-2000;
17-NOV-2000;
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16-MAR-2000;
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AAK85505;
                                                                                                                                                                                                                                                                                        The present invention relates to the isolation of novel human enzyme polypeptides (AAU22915-AAU23814), and the cDNA and genomic sequences encoding them. The enzyme polypeptides of the invention may comprise the functional classes of oxidoreductases, transferases, hydrolases, lyases, isomerases or ligases. The sequences of the invention are useful in the disorders including hyperproliferative disorders (e.g. cancer), immunodeficiency disorders (e.g. AIDS) autoimmune disorders (e.g. cartritis), neurological disorders (e.g. AIDS) autoimmune disorders (e.g. arthaner's disorders (e.g. infectious disorders (e.g. Influencai). The polymucleotides of the infectious disorders (e.g. Influencai). The polymucleotides of the invention can also be used in gene therapy. AAA34685-AA342192 represent DNA sequences encoding for the novel human enzyme polypeptides of the invention. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at fip. WiPo int/pub/published_pot_sequences
                                          Novel polypeptides and polynucleotides useful for diagnosing, preventing,
                                                                                    treating neural, immune system, muscular, reproductive, pulmonary, cardiovascular, renal, proliferative disorders and cancerous diseases.
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Pred. No. 6.6e-112;
0; Mismatches 0; Indels
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                                                                                                                                                                                                                           Disclosure; SEQ ID NO 2001; 1180pp; English.
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1098 ATATATGAGTAAACTTGGTCTGACAGTTACCAATGCTTAATCAGTGAGGCACCTATCTCA 1039
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                                                 GCGATCTGTCTATTTCGTTCATACCCATAGTTGCCTGCAACTCCCCGTCGTGTAGATAACT
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ATATATGAGTAAACTTGGTCTGACAGTTACCAATGCTTAATCAGTGAGGCACCTATCTCA
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20-OCT-2000;
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30-AUG-2000
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Barash SC, Ruben SM (HUMA-) HUMAN GENOME SCI INC Rosen CA,

WPI; 2001-483426/52

Nucleic acids encoding human immune/hematopoietic antigen polypeptides, useful for preventing, diagnosing and/or treating cancers and metastasis.

Disclosure; SEQ ID NO 40317; 3071pp + Sequence Listing; English.

AAK54951 to AAK64702 encode the human immune/haematopoietic antigen (I) amino acid sequences given in AAM82170 to AAM91921. (I) have cytostatic activity, and can be used in gene therapy and vaccine production. (I) proteins and polymucleotides may be used in the prevention, diagnosis and treatment of diseases associated with inappropriate (I) expression. For example, they may be used to treat disorders associated with decreased expression by rectifying mutations of deletions in a patient's genome that affect the activity of (I) by expressing inactive proteins or to polymucleotides may be used to produce the secreted (I), by inserting the nucleic acids into a host cell and culturing the cell to express the protein. (I) proteins and polymucleotides may be used to prevent,

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02-MAR-2000; 2000US-0186350P.
16-MAR-2000; 2000US-0189874P.
18-ARR-2000; 2000US-0199076P.
18-ARR-2000; 2000US-0198123P.
07-JUN-2000; 2000US-025515P.
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                    1098 ATATATGAGTAAACTTGGTCTGACAGTTACCAATGCTTAATCAGTGAGGCACCTATCTCA 1039
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         diagnose and treat immune/haematopoietic-related diseases, especially cancers and cancer metastases of haematopoietic-derived cells. AAK64703 to AAK87694 represent human immune/haemacopoietic antigen genomic sequences from the present invention. AAK54942 to AAK54950 and AAW82169 represent sequences used in the exemplification of the present invention
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                                                                                                                                                        92.4%; Score 462; DB 4; L 99.2%; Pred. No. 6.6e-112; tive 0; Mismatches 0;
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Matches 496; Conservative
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(HUMA-) HUMAN GENOME SCI INC

Ruben SM Rosen CA, Barash SC,

WPI; 2001-483426/52

Nucleic acids encoding human immune/hematopoietic antigen polypeptides, useful for preventing, diagnosing and/or treating cancers and metastasis.

Disclosure; SEQ ID NO 24441; 3071pp + Sequence Listing; English

AAK54951 to AAK64702 encode the human immune/haematopoietic antigen (I)

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amino acid sequences given in AAM82170 to AAM91921. (I) have cytostatic activity, and can be used in gene therapy and vaccine production. (I) proteins and polymucleotides may be used in the prevention diagnosis and treatment of diseases associated with inappropriate (I) expression. For example, they may be used to treat disorders associated with decreased extra affect the activity of (I) by expressing inactive proteins or to supplement the patients own production of (I). Additionally, (I) polymucleotides may be used to produce the secreted (I), by inserting the nucleic acids into a host cell and culturing the cell to express the protein. (I) proteins and polymucleotides may be used to prevent, diagnose and treat immune/haematopoietic-derived cells. AAK84703 to AAK87694 represent human immune/haematopoietic antigen genomic sequences from the present invention. AAK84942 to AAK87590 and AAM82169 represent sequences used in the exemplification of the present invention
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Pred. No. 6.6e-112;
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GenCore version 5.1.6 Copyright (c) 1993 - 2005 Compugen Ltd. OM nucleic - nucleic search, using sw model Run on: April 29, 2005, 02:02:08; Search time 2527 Seconds (without alignments) 7531.514 Million cell updates/sec Perfect score: 1 US-10-043-160-5_COPY_1_500 Sequence: 2 Searched: 34239544 seqs, 19032134700 residues Total number of hits satisfying chosen parameters: 68479088	Minimum DB seq length: 0 Maximum DB seq length: 2000000000	Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries Database: EST:* 1: gb_est:* 2: gb_est:* 3: gb_htc:* 5: gb_est:* 6: gb_est:* 6: gb_est:* 7: gb_est:* 8: gb_gss:* 9: gb_gss:* 9: gb_gss:* 9: gb_gss:* 8:	1 460.4 92.1 758 9 CL422788 CC4422788 CC4422788 CC4422788 CC422768 AC6048 AC6048 AC6048 AC6082893 AC601035 AC601035 AC61035 AC610306 AC61037 AC

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Takasuga,A., Hirotsune,S., Itoh,R., Jitohzono,A., Suzuki,H., Aso,H. and Sugimcho,Y.
Establishment of a high throughput EST sequencing system using poly(A) tail-removed cDNA libraries and determination of 36,000 bovine ESTs
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Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
Bovinae; Bos.
Library constructed by Life Technologies. Investigator providing samples: Jeffrey Green, M.D., NIH^{\prime\prime}
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Animal Genetics Division
Shirakawa Institute of Animal Genetics
Odakura, Nishigo, Nishi-shirakawa, Fukushima 961-8061, Japan
Tel: 81-248-25-5725
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                                                                                          832;
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ENATYOTA; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Enkaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Enkaryota; Metazoa; Chordata; Sciurognathi; Muridae; Murinae; Mus.
CE 1 (bases 1 to 832)
RS NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
AL Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: Gapba-rômail.nih.gov
Contact: Robert Strausberg, Ph.D.
CONTA Library Preparation: Life Technologies, Inc.
CONA Library Preparation: Life Technologies, Inc.
CONA Library Arrayed by: The I.M.A.G.E. Consortium (LINL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov.j coluum: 23
High quality sequence start: 32
High quality sequence start: 32
High quality sequence stop: 823.
Location/Qualifaers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BG923768 832 bp mRNA linear EST 05-JUN-2001
62825893F1 NCI_CGAP_Mam6 Mus musculus cDNA clone IMAGE:4954486 5',
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /sex="female, virgin"
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/dev stage="5 months"
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/lab_host="DH10B"
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/ince="Organ: mammary, vector: pcwv-sports; Site 2: Not1; Cloned unidirectionally.
                                                                                          376
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                                                                                                                                        181 CTCACCGGCTCCAGATTTATCAGCAATAAACCAGCCAGCAGGAAGGGCCGAGAGG 240
                                                                                                                                                                                  436
                                                                                                                                                                                                                              241 TGGTCCTGCAACTTTATCCGCCTCCATCCAGTCTATTAATTGTTGCCGGGAAGCTAGAGT 300
                                                                                                                                                                                                                                                                        496
      261 GCGATCTGTCTATTTCGTTCAT-CCATAGTTGCCTG--ACTCCCCGTCGTGTAGATAACT 317
                                                                            318 ACGATACGGGAGGCTTACCATCTGGCCCCAGTGCTGCAATGATACCGCG-AGACCCACG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         437 TGGTCCTGCAACTTTATCCGCCTCCATCCAGTCTATTAATTGTTGCCGGGAAGCTAGAGT
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                                                  121 ACGATACGGGAGGGCTTACCATCTGGCCCCAGTGCTGCAATGATACCGCGAAGACCCACG
                                                                                                                                                                                                                                                                                                                    301 AAGTAGTTCGCCAGTTAATAGTTTGCGCAACGTTGTTGCCATTGCTGCAGCCATCGTGGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                     557 GICACGCICGICGIIIGGIAIGGCIICAIICAGCICCGGIICCCAACGAICAAGGCGAGI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1. .832
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mus musculus (house mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BG923768.1 GI:14304244
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              mRNA sequence.
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SOURCE
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LOCUS
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AUTHORS
TITLE
JOURNAL
COMMENT
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FEATURES

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and Sugimoto,Y.

Establishment of a high throughput EST sequencing system using poly(A) tail-removed cDNA libraries and determination of 36,000 poly(A) tail-removed cDNA libraries and determination of 36,000 bovine ESTB

LISTOSS4

ID 1171328

Contact: Yoshikazu Sugimoto
Animal Genetics Division
Shirakawa Institute of Animal Genetics
Odakura, Nishigo, Nishi-shirakawa, Fukushima 961-8061, Japan Tel: 81-248-25-5641
Fax: 81-248-25-5641
Fax: 81-248-25-555
Email: kazusugiacocoa ocn.ne.jp
Single pass sequencing.
This clone was obtained from a polyA-deleted cDNA library.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  271
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    331
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 /tissue_type="lung"
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/clone_lib="Bos taurus lung fetus"
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was deleted from a Not1 site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        506 ATATATGAGTAAACTTGGTCTGACAGTTACCAATGCTTAATCAGTGAGGCACCTATCTCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    330 CTCACCGGCTCCAGATTATCAGCAATAAACCAGCCAGCCGGAAGGGCCCAGCGCAGAAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           90 TACATGATCCCCCATGTTGTGCAAAAAAGCGGTTAGCTCCTTCGGTCCTCCGATCGTTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      389 ACGATACGGGAGGCTTACCATCTGGCCCCAGTGCTGCAATGATACCGCG-AGACCCACG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            241 TGGTCCTGCAACTTTATCCGCCTCCATCCAGTCTATTAATTGTTGCCGGGAAGCTAGAGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                210 AAGTAGTTCGCCAGTTAATAGTTTGCGCAACGTTGTTGCCATTGCTACAGGCATCGTGGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TACATGATCCCCCATGTTGTGCAAAAAGCGGTTAGCTCCTTCGGTCCTCCGATC-GTTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAGTAGTTCGCCAGTTAATAGTTTGCGCAACGTTGTTGCCATTGCTGCAGGCATCGTGGT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 449.4; DB 1;
Pred. No. 2.8e-135;
0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                1. .523
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/clone="ElLU035B04"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TCAGAAGTAAGTTGGCCGCAG 500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             30 TCAGAAGTAAGTTGGCCGCAG 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 tch 89.9%; al Similarity 98.8%; 495; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
Matches 495; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              121 ACGATACGGGAGGCTTACCATCTGGCCCCAGTGCTGCAATGATACCGGGAAGACCCACG 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        469
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61 GCGATCTGTCTATTTCGTTCATCCCATAGTTGCCTGCAACTCCCCGTCGTGTAGATAACT 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                241 IGGTCCTGCACTTTATCCGCCTCCATCCAGTCTATTAATTGTTGCCGGGAAGCTAGAGT 300
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               232 AAGTAGTTCGCCAGTTAATAGTTTGCGCAACGTTGTTGCCATTGCTACACAGCATCGTGGT 173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         361 GTCACGCTCGTCGTTTGGTATGGCTTCATTCAGCTCCGGTTCCCAACGATCAAGGCGAGT 420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   172 GTCACGCTCGTCGTTTGGTATGGCTTCATTCAGCTCCGGTTCCCAACGATCAAGGCGAGT 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         421 TACATGATCCCCCATGTTGTGCAAAAAGCGGTTAGCTCCTTCGGTCCTCCGATCGTTGT 480
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      411 ACGATACGGGAGGCCTTACCATCTGGCCCCAGTGCTGCAATGATACCGCG-AGACCCACG 353
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Bos taurus
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalla, Eutheria, Cetartiodactyla, Ruminantia, Pecora, Bovidae,
Bovinae, Bos.
                                                                                                                                                                                /tissue_type="lung"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       301 AAGTAGTTCGCCAGTTAATAGTTTGCGCAACGTTGTTGCCATTGCTGCAGGCATCGTGGT
                                                                                                                                                                                                                                                                                                                                                                                                                                  1 ATATATGAGTAAACTTGGTCTGACAGTTACCAATGCTTAATCAGTGAGGCACCTATCTCA
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                                                                                                                                                                                                                                                                                                                                                                                          Gaps
  4 ;
                                                                                                                                                                                                                                                                                                                                                Length 635;
                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                              Query Match 91.9%; Score 459.4; DB 1; Best Local Similarity 99.8%; Pred. No. 1.6e-138; Matches 494; Conservative 0; Mismatches 2;
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EST.
                                                                                    1. .635
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AV610857/c
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AUTHORS
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CD240106 659 bp mRNA linear EST 14-APR-2004
DTL3P2A4 THP-1 OligodT Library Homo sapiens CDNA, mRNA sequence.
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/note="Vector: PT7BLUEZ blunt cloning vector (Novagen);
Site_1: Smal; Site_2: Smal; The library was prepared from
LPS-Fimulated cell line pre-treated with cycloheximide."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       106 Tricerricar-ccaracritectre--acreecercereragaraacracgaracagagg 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  163 GCTIACCATCTGGCCCCAGTGCTGCAATGATACCGCG-AGACCCACGCTCACGGCTCCA 221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          314 GITAATAGITITGCGCAACGITGTTGCCATTGCTGCAGGCATCGTGGTGTCACGCTCGTCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       74 TTCGTTCATCCCATAGTTGCCTGCAACTCCCCGTCGTGTAGATAACTACGATACGGAGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       134 GCTTACCATCTGGCCCCCAGTGCTGCAATACCGCGAAGACCCACGCTCACCGGCTCCA
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Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
1 (bases 1 to 659)
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                                                                                                                                                                                                                                                                                                                                                                                                                                   CDNA abundance

RNA 10 (4), 747-753 (2004)

CONTact: Khalid S.A Khabar
Interferrons and Cytokines Unit
King Faisal Specialist Hospital and Research Centre
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Tel: 966-1-442-7876
Fax: 966-1-442-7856
Email: khabar@kfshrc.edu.sa.

Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                  Khabar, K.S., Dhalla, M., Al-Haj, L., Bakheet, T., Sy, C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
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98.8%; Pred. No. 4.5e-134;
tive 0; Mismatches 2;
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/organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /mol_type="mRNA"
/db_xref="taxon:9606"
/cell_type="Monocytes"
/cell_line="THP-1"
CAGAAGTAAGTTGGCCGCAG 348
                                                                                                                                                                                                            CD240106.1 GI:38044974
                                                                                                                                                                                                                                                        Homo sapiens (human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 98.8<sup>1</sup>
Matches 481; Conservative
                                                                                                                                                                                                                                                                                                                                                                                               Naemuddin, M.
                                                                                                                                                                                                                                                                             Homo sapiens
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                                                                                                                                                            Ictalurus punctatus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Siluriformes;

Ictaluridae; Ictaluria; Neopterygii; Teleostei; Ostariophysi; Siluriformes;

I (bases 1 to 854)

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        546 AAGTAGTTGGCCAGTTAATAGTTTGCGCAACGTTGTTGCCATTGCTACAGGCATCGTGGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ВМ438950
IpLvr00491 Liver cDNA library Ictalurus punctatus cDNA 5', mRNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /organism="Ictalurus punctatus"
/mol_type="mRNA"
/db xref="texon:7998"
/clone_lib="Liver cDNA_library"
/clone_lib="Liver; Vector: pSport1; Site_1: Not1;
Site_2: Sall"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       5.
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98.6%; Pred. No. 2.3e-134;
iive 0; Mismatches 2;
    mRNA
                                                                                                                                              Ictalurus punctatus (channel catfish)
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                                                                                                     BM438950.1 GI:18460672
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Best Local Similarity 98.6'
Matches 493; Conservative
                                                            sequence.
                                                                                 BM438950
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                                                                                                VERSION
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Bukaryota; Butheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 721)
Homo sapiens genomic DNA, chromosome 21q
Homo sapiens genomic DNA, chromosome 21q
Dubated 1 to 721)
Hattori,M., Ishii,K., Toyoda,A., Shiba,T. and Sakaki,Y.
Direct Submission
L Submission
L Submitted (29-UUI-1998) Masahira Hattori, Kitasato University, Department of Science, JST Sequencing Laboratory; Kitasato 1-15-1, Sagamihara 228, Japan (E-mail:hattori@hgc.ims.u-tokyo.ac.jp, Tel:047-78-9372; Fax:0427-78-9561)
On Feb 5, 1999 this sequence version replaced gi:2826191.
AG004662; Submitted (30-Jan-1998).
                                                                                                                                                                                                                                                                                                              AG011001 721 bp DNA linear GSS 14-APR-1999
Homo sapiens genomic DNA, 21q region, clone: 879G12X91, genomic
    436
                                                                               246
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   377 GGTATGGCTTCATTCAGCTCCGGTTCCCAACGATCAAGGCGAGTTACATGATCCCCATG
                                        357 GGTATGGCTTCATTCAGCTCCGGTTCCCAACGATCAAGGCGAGTTACATGATCCCCCATG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GGCTCCAGATTTATCAGCAATAAACCAGCCAGCCGGAAGGGCCGAGCGCAGAAGTGGTCC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /organism="Homo sapiens"
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/db_xref="taxon:9606"
/chromosome="21"
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/clone="879G12X91"
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AG011001 AG004662
AG011001.1 GI:3357935
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Best Local Similarity 98.84
Matches 488; Conservative
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AG011001/c
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Haplochromis sp. 'red tail sheller'
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Actinopterygii; Neopterygii; Teleostei; Buteleostei; Neoteleostei;
Acanthomorpha; Acanthopterygii; Percomorpha; Perciformes;
Labroidei; Cichlidae; Haplochromis.
  493
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                                          521
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            13.7 TACCATCTGGCCCCAGTGCTGCAATGATACCGCGAAGACCCACGCTCACCGGCTCCAGAT 196
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                 317 AATAGTTTGGGCAACGTTGTTGCCATTGCTGCAGGCATCGTGGTGGTCGTCGCTCGTCGTTT
1 (bases 1 to 626)
Watanabe,M., Kobayashi,N., Shin-i,T., Kohara,Y. and Okada,N.
Orf sequences of cichlid in Lake Victoria are essentially same
Unpublished (2004)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 GGTCTGACAGTTACCAATGCTTAATCAGTGAGGCACCTATCTCAGCGATCTGTCTATTTC
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/mol_type="mRNA"
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/clone="no575f01"
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/dev stagge="varied"
/clone_lib="HREST library"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Contact: Tadasu Shin-i
Center: For Genetic Resource Information
National Institute of Genetics
1111 Yata, Mishima, Shizuoka 411-8540, Japan
Tel: 81-559-81-6856
Email: tshini@genes.nig.ac.jp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       88.9%; Score 444.4; DB 4;
99.0%; Pred. No. 1.3e-133;
ive 0; Mismatches 1;
                                                                                                                                                                                                                                                                     one no575f01, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       tshini@genes.nig.ac.jp.
Location/Qualifiers
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BJ695105.1 GI:46538226
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Best Local Similarity 99.0
Matches 479; Conservative
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BM438846 1013 bp mRNA linear EST 31-JAN-2002 IpLvr00157 Liver cDNA library Ictalurus punctatus cDNA 5', mRNA
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Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Siluriformes;
Ictaluridae; Ictalurus.
1 (bases 1 to 1013)
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Transcriptome of channel catfish (Ictalurus punctatus): initial
analysis of expressed sequence tags from the liver
Unpublished (2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Contact: Liu ZJ
The Fish Molecular Genetics and Biotechnology Laboratory,
The Fish Molecular Genetics and Allied Aquacultures and Program of
and Molecular Biosciences
Auburn University
201 Swingle Hall, Auburn University, Auburn, AL 36849, USA
Tel: 334 844 4054
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                                                                                                   386 GGTATGGCTTCATTCAGCTCCCGGTTCCCAACGATCAAGGCGAGTTACATGATGATCCCCATG
                                                                                                                                                                                     317 AATAGTTTGCGCAACGTTGTTGCCATTGCTGCAGGCATCGTGGTGTCACGCTCGTCGTTT
                    326 AATAGTTTGCGCAACGTTGTTGCCATTGCTACAGGCATCGTGGTGTCACGCTCGTCGTCGTTT
                                                                               377 GGTATGGCTTCATTCAGCTCCGGTTCCCAACGATCAAGGCGAGTTACATGATCCCCCCATG
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/note="Organ: Liver; Vector: pSport1; Site_1: Not1;
Site_2: Sall"
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98.6%; Pred. No. 2.8e-131;
tive 0; Mismatches 1;
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Ictalurus punctatus
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/db_xref="taxon:7998"
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Bukaryota; Metazoa; Chordata; Catarrhini; Hominidae; Homo.
Mammalia; Euthoria; Primates; Catarrhini; Hominidae; Homo.

L (bases 1 to 689)
L Published Only in DataBase (1998)
L Published Only in DataBase (1998)
L 2 (bases 1 to 689)
S Hattori,M., Ishii,K., Toyoda,A., Shiba,T. and Sakaki,Y.
Homo sapiens genomic DNA, chromosome 21q
L Published Only in DataBase (1998)
L 2 (bases 1 to 689)
S Hattori,M., Ishii,K., Toyoda,A., Shiba,T. and Sakaki,Y.
Direct Submission
L Submitted (17-SRP-1998) Masahira Hattori, Kitasato University, Department of Science, JST Sequencing Laboratory; Kitasato 1-15-1, Sagamihara 228, Japan (E-mail:hattori@hgc.ims.u-tokyo.ac.jp, Tel:0427-78-9732, Fax:0427-78-9561)
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                             AG014394 689 bp DNA linear GSS 08-FEB-1999
Homo sapiens genomic DNA, 21q region, clone: B355C245pN18, genomic
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TTCGCCAGTTAATAGTTTGCGCAACGTTGTTGCCATTGCTACAGGGATCGTGGTGTCACG 230
                                                              426
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                                                                                                   229 cicercerriegrarescricaricaecreesgriceaaceareaasesgriacare 170
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         427 ATCCCCCATGTTGTGCAAAAAGCGGTTAGCTCCTTCGGTCCTCCGATCGTTGTCAGAAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GGTCTGACAGTTACCAATGCTTAATCAGTGAGGCACCTATCTCAGCGATCTGTCTATTTC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
/chromesome="21"
/map="21q"
/clone="B355C24SpN18"
                                                                                                                                                                                                                                                                                                                                                           dq 689
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GSS.
                                                                                                                                                                                                                          487 TAAGTTGGCCGCAG 500
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AG014394
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Crassostrea virginica (eastern oyster)
Crassostrea virginica
Crassostrea, Virginica
Enkaryota; Metazoa; Mollusca; Bivalvia; Pteriomorphia; Ostreoida;
Ostreoidea; Ostreidae; Crassostrea.

1 (bases 1 to 819)
Peatman, E., Kucuktas, H., Li, P., He, C., Peng, J., Wei, X. and Liu, Z.
Differentially expressed oyster (Crassostrea virginica) genes after
Unpublished (2003)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               819 bp mRNA linear EST 18-JUN-2003
CVGA00080 Crassostrea virginica Gonad Crassostrea virginica cDNA
CD649375
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Contact: Liu ZJ
The Fish Molecular Genetics and Biotechnology Laboratory,
Department of Fisheries and Allied Aquacultures and Program of Cell
and Molecular Biosciences
Auburn University
203 Swingle Hall, Auburn University, Auburn, AL 36849, USA
                                                                                                                                                                                                     425
                                                                                                                                                        286 GTTCGCCAGTTAATAGTTTGCGCAACGTTGTTGCCATTGCTACAGGCATCGTGGTGTCAC 227
                                                                                                                                                                                                                                                  167
                                                                                                                                                                                                                                                                                              485
                                                                                                                                                                                                                                                                                                                      166 GATCCCCCATGTTGTGCAAAAAAGCGGTTAGCTCCTTCGGTCCTCCGATCGTTGTCAGAA 107
                                                               346 CIGCAACITIAICCGCCICCAICCAGICIAILAAIIGIIGCCGGGAAGCIAGAGIAAGIA 287
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                                                                                                                                                                                                                               226 GCTCGTTGGTTTGGTATGGCTTCATTCAGCTCCGGTTCCCAACGATCAAGGCGAGTTACAT
                                                                                                                                                                                                                                                                                            426 GATCCCCCATGTTGTGCAAAAAGCGGTTAGCTCCTTCGGTCCTCCGATCGTTGTCAGAA
                                                                                                                                                                                                     366 GCTCGTCGTTTGGTATGGCTTCATTCAGCTCCGGTTCCCAACGATCAAGGCGAGTTACAT
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'Coganism="Crassostrea virginica"

/mol type="mRNA"

/db_Xref="taxon:6565"

/db_Xref="taxon:6565"

/clone lib="Crassostrea virginica Gonad"

/note="Organ: Gonad; Vector: pSport1; Site_1: NotI; Site_2: SalI"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Tel: 334 844 4054
Fax: 334 844 9208
Emall: zliu@acesag.auburn.edu
Seg primer: M13 Reverse.
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EST.
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CD649375/c
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1. (bases 1 to 698)
L. Hattori,M., Ishii,K., Toyoda,A., Shiba,T. and Sakaki,Y.
Homo sapiens genomic DNA, chromosome 21q
L. Published Only in DataBase (1998)
E. 2 (bases 1 to 698)
E. 2 (bases 1 to 698)
E. 3 (bases 1 to 698)
Mattori,M., Ishii,K., Toyoda,A., Shiba,T. and Sakaki,Y.
Direct Submission
L. Submitted (06-JUL-1998) Masahira Hattori, Kitasato University, Department of Science, JST Sequencing Laboratory; Kitasato 1-15-1, Sagamihara 228, Japan (B-mail:hattori@hgc.ims.u-tokyo.ac.jp, Tel:0427-78-9732, Fax:0427-78-9561)
On Feb 5, 1999 this sequence version replaced gi:2754689.
AG003787: Submitted (07-Jan-1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     698 bp DNA linear GSS 14-APR-1999
Homo sapiens genomic DNA, 21q region, clone: T485XN, genomic survey
sequence.
                                            360
                                                                                                                                 420
                                                                                                                                                                                                                          479
547
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                66 CTGTCTATTTCGTTCATCCCATAGTTGCCTGCAACTCCCCGTCGTGGATAACTACGAT 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            126 ACGGGAGGGCTTACCATCTGGCCCCAGTGCTGCAATGATACCGCGAAGACCCACGCTCAC 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            406 CGGCTCCAGATTTATCAGCAATAAACCAGCCAGCCGGAAGGGCCCAGCCCAAGAAGTGGTC 347
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      465 Acedeacecriraccarcrecciccaerecrecardaraccece-adacccacercac 407
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                                                                    546 AAGTAGTICGCCAGTIAATAGTITGCGCAACGTIGCTGTIGCTACAGGCAICGTGGT
                                                                                                                                                             486 GTCACGCTCGTCGTTTGGTATGGCTTCATTCAGCTCCGGTTCCCAACGATCAAGGCGAGT
                                                                                                                                                                                                                                                    426 TACATTGATCCCCCCATGTTGTGCAAAAAGCGGTTAGCT-CTTCGGTCCTCCGATCGTTG
606 TGGTCCTGCAACTTTATCCGCCTCCATCCAGTCTATTAATTGTTGCCGGGAAGCTAGAGT
                                                                                                                                 361 GTCACGCTCGTCGTTTGGTATGGCTTCATTCAGCTCCGGTTCCCAACGATCAAGGCGAGT
                                                                                                                                                                                                                        TACA-TGATCCCCCATGTTGTGCAAAAAGCGGTTAGCTCCTTCGGTCCTCCGATCGTTG
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Pred. No. 4.6e-131;
0; Mismatches 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /organism="Homo sapiens"
| Onl type="genomic DNA"
| Ab_xref="taxon:9606"
| Chromosome="21"
| map="21q"
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Best Local Similarity 98.0%;
Matches 485; Conservative
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AG009976/c
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AV610675

AV610675 Bos taurus lung fetus Bos taurus cDNA clone E1LU033H06 3', mRNA sequence.
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Establishment of a high throughput EST sequencing system using poly(A) tail-removed cDNA libraries and determination of 36,000
                                                                                                                80 CATCCCATAGTTGCCTGCAACTCCCCGTCGTGTAGATAACTACGATACGGGGGGCTTAC 139
                                                                                                                                                                                                                                                                                                                 177 TCAGCAATAAACCAGCCAGCCGGAGGCCGAGCGCAGAAGTGGTCCTGCAACTTTATCC 236
                                                                                                                                                                                                                                           118 CATCTGGCCCCAGGGCTGCAATGATACCGCG-AGACCCACGCTCACCAGGCTCCAGATTTA 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   380 ATGGCTTCATTCAGCTCCGGTTCCCAACGATCAAGGCGAGTTACATGATCCCCCATGTTG 439
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
                                                                                                                                                                                                                                                                                                                                                                                                           1 CTGACAGTTACCCAATGCTTAATCAGTGAGGCACCTATCTCAGCGATCTGTCTATTTCGTT
                                                                                                                                                       61 CAT-CCATAGTTGCCTG--ACTCCCGTCGTGTAGATAACTACGATACGGGAGGGCTTAC
                                                                                                                                                                                                  140 CATCTGGCCCCAGTGCTGCAATGATACCGCGAAGACCCACGCTCCAGGCTCCAGATTTA
                                                                                                                                                                                                                                                                                        200 TCAGCAATAAACCAGCCAGCCGGAAGGGCCGAGAGGAGAGTGGTCCTGCAACTTTATCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          297 AGCCCGCGCAACGTTGTCATGCTACAGGCATCGTGGTGTCACGCTCGTCGTTGGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CTGACAGTTACCAATGCTTAATCAGTGAGGCACCTATCTCAGCGATCTGTCTATTTCGTT
                                                                                                                                                                                                                                                                                                                                                                           320 AGTITGCGCAACGTTGTTGCCATTGCTGCAGCATCGTGGTGTCACGCTCGTCGTTTGGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Contact: Yoshikazu Sugimoto
Animal Genetics Division
Shirakawa Institute of Animal Genetics
Odakura, Nishigo, Nishi-shirakawa, Fukushima 961-8061, Japan
Tel: 81-25-5641
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Fax: 81-248-25-5725
Email: kazusugi@cocoa.ocn.ne.jp
Single pass sequencing.
This clone was obtained from a polyA-deleted cDNA library.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Nucleic Acids Res. 29 (22), E108 (2001)
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/db_xref="taxon:9913"
/clone="ElLU031406"
/tissue_type="lung"
/dev_stage="fetus"
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Bos taurus
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AV610675
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CTGGCCCCAGTGCTGCAATGATACCGCG-AGACCCACGCTCACCGGCTCCAGATTTATCA 644
                                                                                                                                                                                                                  TIGCGCAACGITGITGCCATTGCTGCAGGCATCGTGGTGTCACGCTCGTCGTTTGGTATG 382
                                                                                                                                                                                                                                                                                                                                            463 GCTTCATTCAGCTCCGGTTCCCAACGATCAAGGCGAGTTACATGATCCCCCATGTTGTGC 404
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I (bases 1 to 580)

Goh, S.-H., Park, J.-H., Lee, Y.J., Lee, H.G., Yoo, H.-S., Lee, I.-C., Park, J.-H., Kim, Y.-S. and Lee, C.-C.
Gene expression profile and identification of differentially expressed transcripts during human intrathymic T-cell development
                                                                                                                                                                                                                                                                                                                                                                                         /note="Vector: pGEM-T; cDNA was made from total cytoplasmic RNA of sorted human intrathymic CD3-4-8-T-cell, adaptor ligated, amplified with PCR, and cloned
                                                                 GCAATAAACCAGCCAGCCGGAAGGGCCCGAGCGCAGAAGTGGTCCTGCAACTTTATCCGCC
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/mol_type="mRNA"
/db_xref="taxon:9606"
/tissue_type="Thymus"
/cell_type="Thrathymic T-cell"
/dev_stage="CD3-4-8- triple negative stage"
/clone_lib="KRIBB Human TN intrathymic T-cell cDNA
library"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Korea Research Institute of Bioscience and Biotechnology
Oun-dong 52, Yu Sung-Gu, Daejon 305-333, Republic of Korea
Tel: 82-42-860-4473
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 580;
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97.5%; Pred. No. 2.3e-127;
iive 0; Mismatches 8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Email: gohsh@mail.kribb.re.kr
Seq primer: T7
High quality sequence stop: 580
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    by cDNA sequencing analysis
Genomics 70 (1), 1-18 (2000)
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AW063173
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Fax: 82-42-860-4479
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Best Local Similarity 97.5
Matches 464; Conservative
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RESULT 13 AW063173

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Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots,
rosids, eurosids I; Fabales, Fabaceae, Papilionoideae, Trifolieae,
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                                                                                                                                                                                                                                                                                                                                                                 291 ACGATACGGGGGGCTTACCATCTGGCCCCCAGTGCTGCAATGATACCGCG-AGACCCACG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          530 GTCACGCTCGTTGGTTTGGTATGGCTTCATTCAGCTCCGGNTNCCAACGATCAAGGCGAGT
             /clone_lib="Bos taurus lung fetus"
/note="Vector: pZL1; Site_1: Sal1; Site_2: Not1; Poly
was deleted from a Not1 sTte"
                                                                                                                                                                                                         ATATATGAGTAAACTTGGTCTGACAGTTACCAATGCTTAATCAGTGAGGCACCTATCTCA
                                                                                                                                                                                                                                                                               234 GCGATCTGTCTATTTCGTTCAT-CCATAGTTGCCTG--ACTCCCCGTGTGGATAACT
                                                                                                                                                                                                                                                                                                                                ACGATACGGGAGGGCTTACCATCTGGCCCCAGTGCTGCAATGATACCGGCGAAGACCCCACG
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The Samuel Roberts Noble Foundation
The Samuel Roberts Noble Foundation
Tel: 580 224 6650
Fax: 580 224 6652
Email: gdmay@noble.org
Insert Length: 796 Std Error: 0.00
Plate: 018 row: A column: 07
Seq primer: TCACACAGGAAACAGCTATGAC.
                                                                                                        79.4%; Score 396.8; DB 1; 98.0%; Pred. No. 4.5e-118;
                                                                                                                                             0; Mismatches
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Medicago truncatula
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/lab host="DH10B"
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BQ152411.1 GI:20289470
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                                                                                                                                               Conservative
                                                                                                                    Best Local Similarity
Matches 432; Conserv
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/tissue_rypes"seedlings"
/dev_gtage="seedlings"
/dev_gtage="seedlings"
/clone_lib="Irradiated"
/clone_lib="Irradiated"
/notes="Vector: Lambda_22p; Seedlings were exposed either
to l00 gy gamma or 0.5, 1, 5, or l0 kJ/m2 UV irradiation.
Gamma-irradiated samples were harvested at 6, 12, 24 and
48 hours after treatment. UV-irradiated samples were
harvested 24 hours post-treatment. cDNA was prepared
total RNA from each sample. The cDNA was directionally
ligated into the Uni-zap KN vector (Stratagene) and
packaged using the Gigapack III Gold packaging extracts.
Phagemids containing cDNA inserts were in vivo excised
from the recombinant Uni-zAP XR vector using SAAssist
helper phage and the B. coli strain XII-Blue MRF'
(Stratagene). Excised plasmids were plated using SOLR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       120
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                                                     organism="Medicago truncatula"
                                                                                 |mol_type="mRNA"
|db_xref="taxon:3880"
|clone="NF018A071R"
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.ocation/Qualifiers
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Query Match 92.4
Best Local Similarity 99.2
Matches 496; Conservative
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Sequence 13, Appli
Sequence 13, Appli
Patent No. 5182260
Sequence 152, App
Sequence 416, Appl
Sequence 112, Appli
Sequence 9, Appli
Sequence 9, Appli
                                                                                                                                                        April 29, 2005, 02:23:53; Search time 146 Seconds (without alignments) 5603.687 Million cell updates/sec
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/cgn2_6/ptodata/1/ina/SB_COMB.seq:*
/cgn2_6/ptodata/1/ina/SB_COMB.seq:*
/cgn2_6/ptodata/1/ina/RB_COMB.seq:*
/cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
/cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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US-08-758-417A-416
US-08-944-916-12
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US-08-232-463-8
US-08-232-463-9
US-07-834-539A-49
US-08-800-353-49
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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 1.0
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Perfect score:
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periplasmic proteins of prokaryotic microorganisms in the presence of arginine
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ZIP: 22314
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
GURRBWY APPLICATION DATA:
APPLICATION NUMBER: US/08/594,469
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   extraction
US-08-809-513A-8
US-08-586-740A-12
US-08-594-469-1
US-08-594-469-1
US-08-748-716-2
US-08-748-716-2
US-08-73-463-10
US-08-73-463-10
US-08-73-463-10
US-08-75-72-20
US-08-450-257-20
US-08-450-257-20
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US-08-450-233-20
US-08-450-233-20
US-08-233-463-12
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STREET: 625 Slaters Lane - Fourth Floor
CITY: Alexandria
STATE: Virginia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CLASSIFICATION: 435
PRIOR APPLICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: FR 95 01083
FILING DATE: 31-JAN-1995
ATTORNEY/AGENT INFORMATION:
NAME: FICHTER, Richard E
REGISTRATION NUMBER: 26,382
REFERENCE/DOCKET NUMBER: 26,382
RELECOMMUNICATION INFORMATION:
TELEPHORE: (703) 683-1080
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                        ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               : Method for the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 9, Application US/08594469 Patent No. 5700665
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
APPLICANT: LEGOUX, Richard
APPLICANT: MALDONADO, Paul
APPLICANT: MALDONADO, Paul
APPLICANT: SALOME, Marc
TITLE OF INVENTION: Method for
TITLE OF INVENTION: presence
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSE: Becon & Thomas
STREET: 625 Slaters Lane
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH: 1905 base pairs
TYPE: nucleic acid
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Sequence 13, Application US/09202904A

Batent No. 6.95471

GENERAL INFORMATION:
APPLICANT: Habn, Bunneuk
TITLE OF INVENTION: Hepatitis C Surrogate Virus for Testing
TITLE OF INVENTION: Come and Use Thereof
FILE REFERENCE: A32210-PCT-USA 072944 0104
CURRENT APPLICATION NUMBER: US/09/202,904A
PRIOR APPLICATION NUMBER: US/09/202,904A
PRIOR PILING DATE: 1997-06-25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1233 TACATGATCCCCCATGTTGTGCAAAAAGCGGTTAGCTCCTTCGGTCCTCCGATCGTTGT 1292
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Best Local Similarity 99.2%; Pred. No. 1.2e-150;
Matches 496; Conservative 0; Mismatches 0;
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SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 13
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                 REFERENCE/DOCKET NUMBER: REF.
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 683-0500
TELEFAX: (703) 683-1080
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 1905 base pairs
TYPE: nucleic acid
STRANDEDNESS: aingle
TOPOLOGY: linear
                                                                                                                                                                                                                              MOLECULE TYPE: DNA (genomic)
REGISTRATION NUMBER:
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US-09-202-904A-13/c
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Patent No. 5856142
GENERAL INFORMATION:
APPLICANT: LEGOUX, Richard
APPLICANT: ALCOUX, Richard
APPLICANT: SALONE, Marc
APPLICANT: SALONE, Marc
TITLE OF INVENTION: periplasmic proteins of prokaryotic microorganisms in the VMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: Bacon & Thomas
                                                                                                                                                                                                                                                                                                 1053 TGGTCCTGCAACTTTATCCGCCTCCATCCAGTCTATTAATTGTTGCCGGGAAGCTAGAGT 1112
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC comparible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
APPLICATION DATA:
APPLICATION NUMBER: US/08/906,957
FILING DATE: 06-AUG-1997
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           - Fourth Floor
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FILING DATE: 31-JAN-1995
ATTORNEY/AGENT INFORMATION:
NAME: FICHTER, Richard E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 481 CAGAAGTAAGTTGGCCGCAG 500
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/594,469
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CITY: Alexandria
STATE: Virginia
COUNTRY: USA
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                       1566 GCGATCTGTCTATTTCGTTCAT-CCATAGTTGCCTG--ACTCCCCGTCGTGTAGATAACT
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5182260-18
FRECULT 5
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FILLING OF INVENTION: DNA SEQUENCES ENCODING SNAKE VENOM
FINHIBITORS OF PLATELET ACTIVATION PROCESSES FOR PRODUCING
FINHIBITORS ADD. COMPOSITIONS USING THEM
NUMBER OF SEQUENCES: 22
FURNERT APPLICATION DATA:
FILLING DATE: 01-NOV-1899
FRIOR APPLICATION DATA:
FRILING DATE: 01-NOV-1899
FRIOR APPLICATION NUMBER: 303,585
FILLING DATE: 27-JAN-1899
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Pred. No. 1.5e-150;
0; Mismatches 0;
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Matches 496; Conservative
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                                                                                                                                                                 Length 2320;
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                                                          FEATURE:
OTHER INFORMATION: Genetically engineered virus derived from
OTHER INFORMATION: poliovirus and hepatitis C virus
US-09-202-904A-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PAPELICATION MANAGANORE, JOHN M.; JAKUBOWSKI, JOSEPH A.
PAPELICATI: MARAGANORE, JOHN M.; JAKUBOWSKI, JOSEPH A.
TITLE OF INVENTION: DNA SEQUENCES ENCODING SNAKE VENOM
INHIBITORS OF PLATELET ACTIVATION PROCESSES FOR PRODUCING
THOSE INHIBITORS AND COMPOSITIONS USING THEM
NUMBER OF SEQUENCES: 22
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/430,313
FILING DATE: 01-NOV-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 303,585
FILING DATE: 27-JAN-1989
PLING DATE: 27-JAN-1989
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                                                                                                                                                              Query Match
92.4%; Score 462; DB 3; L
Best Local Similarity 99.2%; Pred. No. 1.3e-150;
Matches 496; Conservative 0; Mismatches 0;
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99.2%; Pred. No. 1.5e-150;
iive 0; Mismatches 0;
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                   TYPE: DNA
ORGANISM: Artificial Sequence
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Best Local Similarity 99.2
Matches 496; Conservative
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Pred. No. 1.5e-150;
0; Mismatches 0; Indels
                                                                                        PRILING DATE: 10-DEC-1993
PRIOR APPLICATION NUMBER: US 08/165,699
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/209,741
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/352,322
FILING DATE: 07-DEC-1994
PRIOR APPLICATION NUMBER: US 08/352,322
PRIOR APPLICATION NUMBER: US 08/544,404
FILING DATE: 10-OCT-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/728,463
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/728,463
FILING DATE: 10-OCT-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/US96/16433
FILING DATE: 10-OCT-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/US97/21803
FILING DATE: 02-DEC-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/US97/21803
ATNONEY/AGENT INFORMATION:
NAME: APPLE NAMER: 36,429
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 014643-009040US
TELECOMMUNICATION INFORMATION:
FILING DATE: US 08/161,739
PRIOR APPLICATION DATA:
APPLICATION NIMERAL
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TELERAK: (415) 576-0300
INFORMATION FOR SEQ ID NO: 152:
SEQUENCE CHARACTERISTICS:
LENGTH: 3122 base pairs
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Best Local Similarity
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                                            1682 CTCACCGGCTCCAGATTTATCAGCAATAAACCAGCCGGAAGGCCCGAAGGGCCGAGAGG 1741
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               301 AAGTAGTTCGCCAGTTAATAGTTTGCGCAACGTTGTTGCCATTGCTGCAGGCATCGTGGT
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                                                                                                                  241 IGGICCIGCAACITIATCCGCCICCAICCAGICIATAATIGITGCCGGGAAGCIAGAGI
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APPLICANT: Lonberg, Nils
APPLICANT: Lonberg, Nils
APPLICANT: Kay, Robert M.
TITLE OF INVENTION: Transgenic No. 6255458-Human Animals for
TITLE OF INVENTION: Producing Heterologous Antibodies
NUMBER OF SEQUENCES: 421
CORRESPONDENCE ADDRESS:
ADDRESSED: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
GITY: San Francisco
STATE: California
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
SOFTWARE: Patentin Release #1.0, Version #1.30
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US 07/810,279
FILING DATE: 17-DEC-1991
APPLICATION NUMBER: US 07/853,408
FILING DATE: 18-MAR-1992
PRIOR APPLICATION NUMBER: US 07/950,668
FILING DATE: 23-JUN-1992
PRIOR APPLICATION NUMBER: US 07/904,068
FILING DATE: 23-JUN-1992
PRIOR APPLICATION NUMBER: US 07/990,860
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FILING DATE: 16-DEC-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/053,131
FILING DATE: 26-APR-1993
PRIOR APPLICATION NUMBER: US 08/096,762
FILING DATE: 22-UUL-1993
FRILNG DATE: 22-UUL-1993
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FILING DATE: 18-NOV-1993
PRIOR APPLICATION DATA:
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Patent No. 6255458
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2446 TACATGATCCCCCATGTTGTGCAAAAAAGCGGTTAGCTCCTTCGGTCCTCCGATCGTTGT 2505
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                                                                                                                                                           2030 ATATATGAGTAAACTTGGTCTGACAGTTACCAATGCTTAATCAGTGAGGCACCTATCTCA
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                                                       Gaps
                                                       4
Length 3122;
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APPLICANT: Goryshin, Igor Y
APPLICANT: York, Dona L
APPLICANT: Word C
CONRESPONDENCE ADDRESS: 13
CONNERSIE: South Pinckney Street
CITY: Madison
STATE: WI
COUNTRY: USA
ZIP: 53703
COMPUTER: IBM PC Compatible
COMPUTER: IBM PC Compatible
COMPUTER: IBM PC Compatible
COMPUTER: IBM PC Compatible
COMPUTER: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATE:
APPLICATION NUMBER: US/08/944,916
                                                    Indels
Query Match 92.4%; Score 462; DB 3; 1
Best Local Similarity 99.2%; Pred. No. 1.5e-150;
Matches 496; Conservative 0; Mismatches 0;
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CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/814,877
FILING DATE: 09-SER-1996
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 12, Application US/08944916
Patent No. 5948622
GENERAL INFORMATION:
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                                                    rccrccarcarrar 2505
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Kay, Robert M.
TITLE OF INVENTION: Transgenic No. 6300129-Human Animals for Producing Heterologous Antibodies
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM FC compatible
OCRRATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
                                                    2446 TACATGATCCCCCATGTTGTGCAAAAAGCGGTTAGCTCCTTCGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQUENCES: 417
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: Serafini, Andrew T.
REGISTRATION NUMBER: 41,303
REFERENCE/DOCKET NUMBER: 014643-009030US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/758,417A
FILING DATE: 02-Dec-1996
CLASSIPICATION CURROWN-
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/728,463
FILING DATE: 10-OCT-1995
APPLICATION NUMBER: US 08/544,404
FILING DATE: 07-DEC-1995
APPLICATION NUMBER: US 08/352,322
FILING DATE: 07-DEC-1994
APPLICATION NUMBER: US 08/209,741
FILING DATE: 09-MAR-1994
APPLICATION NUMBER: US 08/209,741
FILING DATE: 09-MAR-1994
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APPLICATION NUMBER: US 08/161,739
FILING DATE: 03-DEC-1993
APPLICATION NUMBER: US 08/155,301
FILING DATE: 18-NOV-1993
APPLICATION NUMBER: US 08/096,762
FILING DATE: 22-UL-1993
APPLICATION NUMBER: US 08/053,131
FILING DATE: 26-APR-1993
FILING DATE: 16-DEC-1992
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MOLECULE TYPE: DNA

SEQUENCE DESCRIPTION: SEQ ID NO: 416:
US-08-758-417A-416
                                                                                                                                                                                                                                                                                     Sequence 416, Application US/08758417A Patent No. 6300129 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
                                                                                                                                                        2506 cagaagraagrigeceedag 2525
                                                                                                         481 CAGAAGTAAGTTGGCCGCAG 500
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TYPE: nucleic acid
STRANDEDNESS: single
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SEQUENCE CHARACTERISTICS:
  421
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2901 CAGAAGTAAGTTGGCCGCAG 2920
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      CURRENT FILING DATE: 1998-04-10
                                                                                                                                                                                                                                              Query Match
Best Local Similarity 99.2%;
Matches 496; Conservative
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                                                                                                                                                         TYPE: DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        421 TACATGATCCCCCATGTTGTGCAAAAAGCGGTTAGCTCCTTCGGTCCTCCGATCGTTGT
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Batent No. 6365347
GENERAL INFORMATION:
APPLICANT: Mirray, Andrew W.
APPLICANT: Smith, Dana L.
APPLICANT: Sorger, Peter K.
APPLICANT: Sorger, Peter K.
APPLICANT: NO. 6365347man, Thea C.
TITLE OF INVENTION: METHODS FOR IDENTIFYING DISRUPTORS OF BIOLOGICAL
TITLE OF INVENTION: PATHWAYS USING GENETIC SELECTION
FILE REPERENCE: 30432.1/USIS
CURRENT APPLICATION NUMBER: US/09/058,483A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   4,
                                                                                                                                                                                                                                                                                                                                                                                                                     Length 3418;
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
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92.4%; Score 462; DB 2; L
Best Local Similarity 99.2%; Pred. No. 1.6e-150;
Matches 496; Conservative 0; Mismatches 0;
                                                                                                                                                                TELEFAX: 608-251-9166
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 3418 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: circular
MOLECULE TYPE: other nucleic acid
DESCRIPTION: /desc = "Plasmid pRZ7075"
                FILING DATE: 02-MAY-1997
TATORNEY/AGENT INFORMATION:
NAME: Berson, Bennett J
REGISTRATION NUMBER: 37094
REFRERENCE/POCKET NUMBER: 960296.94916
TELECOMMUNICATION INFORMATION:
TELEPHONE: 608/251-5000
US 08/850,880
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APPLICATION NUMBER:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            241 IGGICCIGCAACTITAICCGCCTCCAICCAGICTAITAAITGITGCCGGGAAGCTAGAGT
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                                                                                                                                                                                                                                                                                   Length 3516;
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Patent No. 5670367
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: DORNER, F.
APPLICANT: PALKNER, F. G.
ITILE OF INVENTION: RECOMBINANT FOWLPOX VIRUS
NUMBER OF SEQUENCES: 52
CORRESPONDENCE ADDRESS:
ADDRESSEE: Folley & Lardner
STREET: 1800 Diagonal Road, Suite 500
CITY: Alexandria
                                                                                                                                                                                             ; ORGANISM: nucleic acid sequence of PSF248 plasmid US-09-058-483-9
                                                                                                                                                                                                                                                                                Score 462; DB 3;
Pred. No. 1.6e-150;
0; Mismatches 0;
EARLIER APPLICATION NUMBER: 06/835,727
EARLIER FILING DATE: 1997-04-11
NUMBER OF SEQ ID NOS: 18
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 9
LENGTH: 3516
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COUNTRY: USA
ZIP. 22313-0299
COMPUTER READABLE FORM:
MEDIUM TYPE: FLOSPDY disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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GENERAL INFORMATION
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     92.4%; Score 462; DB 1; Length 3656; 99.2%; Pred. No. 1.7e-150; tive 0; Mismatches 0; Indels
Patentin Release #1.0, Version #1.25
             CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/232,463
FILING DATE:
CLASSIFICATION DATA:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/935,313
FILING DATE:
APPLICATION NUMBER: EP 91 114 300.6
FILING DATE: 26-AUG-1991
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
REPERRENCE/DOCKET UNMBER: 30472/114 IMMU
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 836-9300
TELEFAX: (703) 836-9300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2266 CAGAAGTAAGTTGGCCGCAG 2247
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TELEX: 899149
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 3656 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 92.4
Best Local Similarity 99.2
Matches 496; Conservative
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  SOFTWARE:
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US-08-232-463-9/c ; Sequence 9, Application US/08232463 ; Patent No. 5670367

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CTCACCGGCTCCAGATTTATCAGCAATAAACCAGCCGGAAGGGCCGAGCGCAGAAG
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                                                                                                                                                                                                                                                                                                               MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/232,463
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/935,313
APPLICANT: DORNER, F.
APPLICANT: SCHEIFLINGER, F.
APPLICANT: SCHEIFLINGER, F.
APPLICANT: PLAKNER, F. G.
TITLE OF INVENTION: RECOMBINANT FOWLPOX VIRUS
NUMBER OF SEQUENCES: 52
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           29,768
RR: 30472/114 IMMU
                                                                                                                                              ADDRESSEE: Foley & Lardner
STREET: 1800 Diagonal Road, Suite 500
CITY: Alexandria
STATE: VA
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATE:
FILING DATE:
APPLICATION NUMBER: EP 91 114 300.6
FILING DATE: 26-AUG-1991
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 30472/114
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703)836-9300
TELEFAX: (703)633-4109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEFAA:
TELEX: 899149
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 3688 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                              COUNTRY: USA
ZIP: 22313-0299
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        IMMEDIATE SOURCE
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2961
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 49, Application US/08800353
; Patent No. 5874299;
GENERAL INFORMATION:
; APPLICANT: Lonberg, Nils
; APPLICANT: Kay, Robert M.
; TITLE OF INVENTION: Transgenic No. 5874299-Human Animals Capable of
; TITLE OF INVENTION: Producing Heterologous Antibodies
; NUMBER OF SEQUENCES: 77
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: William M. Smith
; STREET: One Market Plaza, Steuart Tower, Suite 2000
; STREET: California
; COUNTRY: USA
                                                                    2842 IGGICCIGCAACTITAICCGCCTCCAICTATTAATIGTGCCGGGAAGCIAGAGT
                                                                                                                                                                               2902 AAGTAGTTCGCCAGTTAATAGTTTGCGCAACGTTGTTGCCATTGCTGCAGGCATCGTGGT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: PatentIn Release #1.0, Version #1.25 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/800,353 FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
92.4%; Score 462; DB 2; 1
Best Local Similarity 99.2%; Pred. No. 1.7e-150;
Matches 496; Conservative ·0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/834,539
FILING DATE: 1992-02-05
ATTOCNEY/AGENT INFORMATION:
NAME: Smith, William M.
REGISTRATION NUMBER: 30,223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ZIP: 94105
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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TELECOMMUNICATION INFORMATION
TELEPHONE: 415-543-9600
TELEFAX: 415-543-5043
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-800-353-49
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EDNESS: single
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Sequence 49, Application US/07834539A
GENERAL INFORMATION:
APPLICANT: Lonberg, Nils
APPLICANT: Kay, Robert M.
TITLE OF INVENTION: Transgenic Non-Human Animals Capable of TITLE OF INVENTION: Producing Heterologous Antibodies
ITITLE OF INVENTION: Producing Heterologous Antibodies
NUMBER OF SEQUENCES: 77
CORRESPONDENCE ADDRESS:
ADDRESSEE: William M. Smith
STREET: One Market Plaza, Steuart Tower, Suite 2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
92.4%; Score 462; DB 1; Length 3698;
Best Local Similarity 99.2%; Pred. No. 1.7e-150;
Matches 496; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/834,539A
FILING DATE: 1992-02-05
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATTORNEY/AGENT INFORMATION:
NAME: Smith, William M.
REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 14643-5
TELEPHONE: 415-543-9600
                                                                                                                                                                                                                            2298 CAGAAGTAAGTTGGCCGCAG 2279
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COMPUTER READABLE FORM:
MEDIUM TYPE: Flopy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                               481 CAGAAGTAAGTTGGCCGCAG 500
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INFORMATION FOR SEQ ID NO: 49:
SEQUENCE CHARACTERISTICS:
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MOLECULE TYPE: DNA (genomic)
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TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STREET: One Market P
CITY: San Francisco
STATE: California
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             USA
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Satent No. 5661016

GENERAL INFORMATION:
APPLICANT: Lonberg, Nils
APPLICANT: Kay, Robert M.
TITLE OF INVENTION: Transgenic No. 5661016-Human Animals for TITLE OF INVENTION: Transgenic No. 5661016-Human Animals for TITLE OF INVENTION: Producing Heterologous Antibodies
NUMBER OF SEQUENCES: 197
CORRESPONDENCE ADDRESS:
ADDRESSER: Townsend and Townsend Khourie and Crew
STREET: One Market Plaza, Steuart Tower, Suite 200
CITY: San Francisco
STATE: California
COUNTRY: USA
                                                              Score 462; DB 5; Length 3698;
Pred. No. 1.7e-150;
0; Mismatches 0; Indels 4
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COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: ISM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PSTENTIN Release #1.0, Ve:
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/053,131
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ON: 800
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APPLICATION NUMBER: US 07/990,860
FILING DATE: 16-DEC-1992
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; MOLECULE TYPE: DNA (genomic) PCT-US92-06185-49
                                                                     Query Match
Best Local Similarity 99.2%;
Matches 496; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE: 26 CLASSIFICATION:
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US-08-053-131-120
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  2606 ATATATGAGTAAACTTGGTCTGACAGTTACCAATGCTTAATCAGTGAGGCACCTATCTCA 2665
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Sequence 49, Application PC/TUS9206185

GENERAL INFORMATION:
APPLICANT: London
APPLICANT: Kay, Robert M.
TITLE OF INVENTION: Transgenic Non-Human Animals Capable of
TITLE OF INVENTION: Producing Heterologous Antibodies
NUMBER OF SEQUENCES: 75
CORRESPONDENCE ADDRESSE:
ADDRESSEE: William M. Smith
STREET: One Market Plaza, Steuart Tower, Suite 2000
CITY: San Francisco
CITY: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SUFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION UNMER: PCT/US92/06185
FILING DATE: 19910828
VITORNEY: PCT/US92/06185
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MEDIUM TYPE: Floppy disk
CMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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NAME: Smith, william M.
REGISTRATION NUMBER: 97554
REFERENCE/DOCKET NUMBER: 146.
TELECOMUNICATION INFORMATION:
TELECHONE: 415-543-9600
TELEPAX: 415-543-9601
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SEQUENCE CHARACTERISTICS:
LENGTH: 3698 base pairs
TYPE: NUCLEIC ACID
STRANDEDNESS: single
TOPOLOGY: linear
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2607 ATATATGAGTAAACTIGGTCTGACAGTTACCAATGCTTAATCAGGGAGCACCTATCTCA 2666
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 92.4%; Score 462; DB 1; Length 3699; Best Local Similarity 99.2%; Pred. No. 1.7e-150; Matches 496; Conservative 0; Mismatches 0; Indels
                         FILING DATE: 17-DEC-1991
FILING DATE: 17-DEC-1991
FRIOR APPLICATION NUMBER: US 07/810,279
FRIOR APPLICATION DATE: US 07/853,408
FILING DATE: 18-MAR-1992
ATTORNEY, AGENT INFORMATION:
NAME: SMith, William M.
REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 14643-9-3
FREFERENCE/DOCKET NUMBER: 14643-9-3
FREFERENCE/DOCKET NUMBER: 14643-9-3
FREFERENCE/DOCKET NUMBER: 126-240
TELECOMMUNICATION INFORMATION:
TELEPAX: 415-326-2402
TELECOMMUNICATION SEQ ID NO: 120: SEQUENCE CHARACTERISTICS:
LENGTH: 3699 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLLOGY: linear
NO-LECULE TYPE: DNA (Genomic)
US-08-053-131-120
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PRIOR APPLICATION DATA:
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Sequence 4, Appli Sequence 1, Appli Sequence 5, Appli Sequence 5, Appli Sequence 2, Appli Sequence 2, Appli Sequence 2, Appli

Sequence 22, Appl Sequence 14, Appl Sequence 13, Appli Sequence 3, Appli Sequence 7, Appli Sequence 7, Appli Sequence 7, Appli Sequence 16, Appli Sequence 15, Appli Sequence 15, Appli Sequence 15, Appli Sequence 15, Appli Sequence 11, Appli Sequence 13, Appli Sequence 11, Appli Sequence 13, Appli Sequence 11, Appli Sequence 13, Appli Sequence 11, Appli

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Database

Searched:

Title: Perfect score:

Sequence:

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Run on:

Scoring table:

Sequence 11, Sequence 20, Sequence 19, Sequence

Length 43228;

Score

Result No.

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Sequence 5, Application US/10043160
| Sequence 5, Application US/10043160
| Sequence 5, Application Wo. US20040170952A1
| GENERAL INFORMATION:
| APPLICANT: ZORONG RINA
| APPLICANT: ZORONG RINA
| APPLICANT: CHAUSE, ANNE-MARIE
| TITLE OF INVENTION: REAGENTS AND METHODS FOR DETECTING GENES RELATED TO
| TITLE OF INVENTION: MAJOR HISTOCOMPATIBILITY COMPLEX OF DOMESTIC FOWL, SUCH
| TITLE OF INVENTION: MAJOR HISTOCOMPATIBILITY COMPLEX OF DOMESTIC FOWL, SUCH
| TITLE OF INVENTION: AS CHICKEN
| FILE REFERENCE: 1721-22
| CURRENT FILING DATE: 2002-01-14
| PRIOR PILING DATE: 2002-01-14
| PRIOR PILING DATE: 1998-11-23
| PRIOR PILING DATE: 1998-11-23
| PRIOR PILING DATE: 1998-11-21
| PRIOR PILING DATE: 1999-11-21
| NUMBER OF SEQ ID NOS: 54
| SOFTWARE: PATENTIN VEY: 2.1
| SEQ ID NO S: 54
| SEG ID NO S: 54
| SEG ID NO S: 54
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OTHER INFORMATION: "n" represents a, t, c, g, other or unknown
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Pred. No. 6.1e-162;
                                        1 US-10-240-532-5

3 US-10-240-532-5

1 US-10-14-03-30

1 US-08-91-14-08-22

1 US-10-161-403-32

1 US-10-161-408-22

1 US-10-742-634-14

1 US-10-742-634-14

1 US-10-742-634-14

1 US-10-742-634-14

1 US-10-740-532-3

1 US-10-240-532-3

1 US-10-240-527A-7

1 US-10-240-527A-7

1 US-10-240-532-15

2 US-10-240-532-15

3 US-10-240-532-15

3 US-10-333-443-1

4 US-10-333-443-1

1 US-10-333-43-1

1 US-10-333-443-1

1 US-10-240-532-13

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US-10-622-220-20
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ORGANISM: Gallus sp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
 LENGTH: 43228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-10-043-160-5
 Sequence 5, Appli
Sequence 577, Ap
Sequence 5577, Ap
Sequence 1456, Ap
Sequence 1462, Ap
Sequence 570, Ap
Sequence 5572, Ap
Sequence 5600, Ap
Sequence 5600, Ap
                                                                                                                    (without alignments)
1182.534 Million cell updates/sec
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(cgn2_6/ptodata/2/pubpna/US07_PUBCOMB.seq:*
(cgn2_6/ptodata/2/pubpna/US06_PUBCOMB.seq:*
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(cgn2_6/ptodata/2/pubpna/US07_NEW_PUB.seq:*
(cgn2_6/ptodata/2/pubpna/US08_PUBCOMB.seq:*
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(cgn2_6/ptodata/2/pubpna/US0B_PUBCOMB.seq:*
                                                                                                   April 29, 2005, 03:41:23 ; Search time 2574 Seconds
               GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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5 US-09-164-891-5577

US-09-764-891-5677

US-09-764-868-1456

US-09-764-868-1450

US-09-764-868-1450

US-09-764-868-15570

US-09-764-891-5570

US-09-764-891-5570

US-09-764-891-5570

US-09-764-891-5570

US-09-764-891-5600

US-09-764-891-5600

US-09-764-891-5600
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Maximum Match 100%
Listing first 45 summaries
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Gapop 10.0 , Gapext 1.0
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Maximum DB seq length: 200000000
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120 ACGATACGGGAGGCTTACCATCTGGCCCCAGTGCTGCAATGATACCGCG-AGACCCAGG	181 CTCACCGCTCCAGATTATCAGCAATAACCAGCCGGCGGAGGGCCGAGGAGGAGGAGGAGGAGGAG	Db 239 TGGTCCTGCAACTTTATCCGCCTCCATCCAGTCTATTAATTGTTGCCGGGAAGCTAGAT 298 Qy 301 AAGTAGTTGCCCACTTAATAGTTTGCGCAACGTTGTTGCCATTGCTGCAGCATCGTGGT 360	361 GTCACGTCGTTGTTAGGTTTCATTCACTCGGTTCCCATGCTGCAACGTTCAAGGCAACGTTCAAGGCAACATCAAGGCAAGATCAAGGCAAGATCAAGGCAAGATCAAGAAGAAGAATCAAGAAGAAGAATCAAGAAGAATCAAGAAGAAGAATCAAGAAGAAGAATCAAGAAGAAAGA	421 TACATGATCCCCCATGTGTGTGAAAAAGCGGTTAGCTCCTTCGGTCCTCCGATCGTTGT 421 TACATGATCCCCCATGTTGTGCAAAAAAGCGGTTAGGTCCTTCGGTCCTCCGATCGTTGT 410 TACATGATCCTCCTATGTTGTGCAAAAAAAGCGGTTAGGTCCTCCGATCCTTGT 410 TACATGATCCTCCTATGTTGTGTAAAAAAAGCGGTTCTTCGTTCTTCTTCTTTGTTTG	481 CAGAAGTAGGCCGCAG 500	DD 479 CAGANGIANGIIGGCCGCAG 490 RESULT 3	US-09-764-891-55/7/C ; Sequence 5577, Application US/09764891 ; Publication No. US20030077808A1 ; GENERAL INFORMATION:	; APPLICANT: Rosen et al.; TITLE OF INVESTION: Nucleic Acids, Proteins, and Antibodies; FILE REFERENCE: PC006; CURRENT APPLICATION NUMBER: US/09/764,891	CURRANIS FALLS DAILS 1201-01-17; Prior application data removed - consult PALM or file wrapper NUMBER OF SEQ ID NOS: 10231 ; SOFTWARE: PatentIn Ver. 2.0 ; SEQ ID NO 5577 ; LENGTH: 2212 ; TYPE: DNA ; TYPE: DNA	US-09-764-891-5577 Query Match Query Match 92.4%; Score 462; DB 10; Length 2212; Best Local Similarity 99.2%; Pred. No. 2.6e-149; Matched Act. Concerns: No. 2.6e-149; Matched Act. Concerns: No. 2.6e-149;	TARACTTGGTCTGACGATACCAATGCTTAATCAGTGAGGCACCTATCTCA 60	OY 61 GCGATCTGTCTATTCGTTCATCCCATAGTTGCCTGCAACTCCCCGTGGTGTAGATAACT 120	121 ACGATACGGGAGGGTTACCATCTGGCCCCAGTGCTGCAATGATACCGCGAAGACCCACG 		Qy 241 TGGTCCTGCAACTTTATCCGCCTCCAGTCTATTAATTGTTGCGGGAAGCTAGGT 300	
Matches 500; Conservative 0; Mismatches 0; Indels 0; Gaps 0;		QY 121 ACGATACGGGAGGCTTACCATCTGGCCCCAGTGCTGCAATGATACCGCGAAGACCCACG 180 Db 121 ACGATACGGGAGGCTTACCATCTGGCCCCAGTGCTGCAATGATACCGCGAAGACCCACG 180	Oy 181 CTCACCGGCTCCAGATTATCAGCAATAAACCAGCCGGAAGGCCGAGCGCAGAGG 240	Qy 241 TGGTCCTGCAACTTTATCCGCCTCCATCCAGTCTATTAATTGTTGCCGGGAAGCTAGAGT 300	OY 301 AAGTAGTTCGCCAGTTAATAGTTTGCGCAACGTTGTTGCTGCTGCAGCCATCGTGGT 360	Qy 361 GTCACGCTCGTTTGGTATGGCTTCATTCAGCTTCCCAACGATCAAGGCGAGT 420	OY 421 TACATGATCCCCCATGTTGTGCAAAAAAGCGGTTAGGTCCTCCGATCGTTGT 480 Db 421 TACATGATCCCCCATGTTGTGCAAAAAAGCGGTTAGGTCCTTCGGTCCTCCGATGTTGT 480	Qy 481 CAGAAGTAAGTIGGCGGCAG 500 Db 481 CAGAAGTAAGTIGGCCGCAG 500	RESULT 2 US-10-182-616-11 US-10-182-616-11 ; Sequence 11, Application US/10182616 ; Publication No. US20030159184A1 ; GENERAL INFORMATION: ; APPLICANT: Sakata Seed Corporation et al	; TITLE OF INVENTION: Methods and Constructs for Plant Transformation; FILE REFERENCE: 78592-3; CURRENT APPLICATION NUMBER: US/10/182,616; CURRENT FILING DATE: 2002-08-01	SOFTWARE: Patentin ver SEQ ID NO 11 LENGTH: 1086 TYPE: DNA	 COGANISM: Artificial Sequence FERATURE: OTHER INFORMATION: Ampicillin resistance gene: pBR322 GenBank Accession No. US200301 OTHER INFORMATION: 3265-4350 	Obery Match Query Match Best Local Similarity 99.2%; Pred. No. 1.9e-149; Matches 496; Conservative 0; Mismatches 0; Indels 4; Gaps		Qy 61 GCGATCTGTCTATTCGTTCATCCCATAGTTGCCTGCAACTCCCCGTCGTAGATAACT 120	Qy 121 ACGATACGGGAGGCTTACCATCTGGCCCCAGTGCTGCAATGATACCGCGAAGACCCACG 180

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                                                                                                                    742 GTCACGCTCGTTCGTTTGGTATGGCTTCATTCAGCTCCCGGTTCCCAACGATCAAGGCGAGT
                                                                                                421 TACATGATCCCCCATGTTGTGCAAAAAAGCGGTTAGCTCCTTCGGTCCTCCGATCGTTGT
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                                                                                                                                                                                                                                                                                        Sequence 5607, Application US/09764891
Publication No. US20030077808A1
GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies FILE REFERENCE: PCO06
CURRENT APPLICATION NUMBER: US/09/764,891
CURRENT FILING DATE: 2001-01-17
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Matches 496; Conservative
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CORGANISM: Homo sapiens
US-09-764-891-5607
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                                                                               APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REFERENCE: PT232
CURRENT APPLICATION NUMBER: US/09/764,868
CURRENT FILING DATE: 2001-01-17
Prior application data removed - refer to PALM or file wrapper NUMBER OF SEQ ID NOS: 1510
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 1456
LENGTH: 2213
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TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REFERENCE: PTZ32
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Pred. No. 2.6e-149;
0; Mismatches 0;
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Patent No. US20020168711A1
GENERAL INFORMATION:
Sequence 1456, Application US/09764868 Patent No. US20020168711A1 GENERAL INFORMATION:
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; Publication No. US20030077808A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: NUCLEIC Acids, Proteins, and Antibodies
; TITLE OF INVENTION: NUMBER: US/09/764,891
; CURRENT FILING DATE: 2001-01-17
; Prior application data removed - consult PALM or file wrapper
; SOFTWARE: Patentin Ver. 2.0
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 5570
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llarity 99.2%; Pred. No. 2.6e-149;
Conservative 0; Mismatches 0; Indels 4
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Pred. No. 2.6e-149;
0; Mismatches 0;
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                                                                                           92.4%;
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Best Local Similarity 99.2°
Matches 496; Conservative
SOFTWARE: Patentin Ver.
SEQ ID NO 1462
LENGTH: 2213
                                    TYPE: DNA
ORGANISM: Homo sapiens
US-09-764-868-1462
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US-09-764-891-5570
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Best Local Similarity
Matches 496; Conserv
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Publication No. US20030077808A1
GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REPERENCE: PC006
CURRENT APPLICATION NUMBER: US/09/764,891
Prior application data removed - consult PALM or file wrapper
NUMBER OF SEQ ID NOS: 10231
SOFTWARE: PatentIn Ver. 2.0
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Pred. No. 2.6e-149;
0; Mismatches 0;
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Best Local Similarity 99.2%;
Matches 496; Conservative C
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; ORGANISM: Homo sapiens
US-09-764-891-5572
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LENGTH: 2213
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Pred. No. 2.6e-149;
0; Mismatches 0;
                                                                     CAGAAGTAAGTTGGCCGCAG 500
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; Sequence 1, Application US/09948939
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US-09-764-891-5602
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Best Local Similarity
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1098 ATATATGAGTAAACTTGGTCTGACAGTTACCAATGCTTAATCAGTGAGGCACCTATCTCA
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                                         GTCACGCTCGTCGTTTGGTATGGCTTCATTCAGCTCCGGTTCCCCAACGATCAAGGCGAGT
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) Sequence 5600, Application US/09764891
; Publication No. US20030077808A1
; GENERAL INFORMATION:
APPLICANT: Rosen et al.
; TILLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REPRENCE: PCOOG
; CURRENT APPLICATION NUMBER: US/09/764,891
; CURRENT PILING DATE: 2001-01-17
; Prior application date removed - consult PALM or file wrapper
NUMBER OF SEQ ID NOS: 10231
; SEQ ID NO 5600
; LENGTH: 2213
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          92.4%; Score 462; DB 10; Length 2213; 99.2%; Pred. No. 2.6e-149; ive 0; Mismatches 0; Indels 4
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Matches 496; Conservative
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FILE REFERENCE: 3005-C
CURRENT APPLICATION NUMBER: US/10/324,493
CURRENT FILING DATE: 2002-12-19
PRIOR APPLICATION NUMBER: US/09/847,816
PRIOR FILING DATE: 2001-05-01
PRIOR FILING DATE: 2000-05-26
PRIOR FILING DATE: 2000-05-26
PRIOR PILING DATE: 2000-05-26
PRIOR PILING DATE: 2000-09-19
PRIOR PILING DATE: 2000-09-19
PRIOR PILING DATE: 2000-09-19
PRIOR PILING DATE: 2001-02-15
NUMBER OF SEQ ID NOS: 26
SOFTWARE: PATCHIN VORTSION 3.0
SEQ ID NO 4
LENGTH: 3159
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Publication No. US20030124523A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                         TYPE: DNA
ORGANISM: Artificial Sequence
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Publication No. US20030124121A1
GENERAL INFORMATION:
APPLICANT: Pluenneke, John
TITLE OF INVENTION: USE OF INTERLEUKIN-4 ANTAGONISTS AND COMPOSITIONS THEREOF
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                                APPLICANT: KORMAN, Alan J.
APPLICANT: Halk, Edward L.
APPLICANT: Halk, Edward L.
APPLICANT: Lonberg, Nils
APPLICANT: Medarex, Inc.
ITILE OF INVENTION: Human CTLA-4 Antibodies and Their Uses
FILE REPREMENT = 0.01620US
CURRENT APPLICATION NUMBER: US/09/948,939
CURRENT PILING DATE: 2001-12-18
PRIOR APPLICATION NUMBER: US 60/150,452
PRIOR PILING DATE: 199-08-24
PRIOR FILING DATE: 2000-08-24
NUMBER OF SEQ ID NOS: 41
SOFTWARE: PARCHIN Ver: 2.1
SEQ ID NO 1
LENGTH: 3159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
92.4%; Score 462; DB 9; Length 3159;
Best Local Similarity 99.2%; Pred. No. 3.1e-149;
Matches 496; Conservative 0; Mismatches 0; Indels
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  Publication No. US20020086014A1
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ORGANISM: Artificial Sequence
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                                                                                                                                           Gaps
                                                                                                                                        4.
                                                                                       Length 3159;
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                                                                            Ouery Match 92.4%; Score 462; DB 15;
Best Local Similarity 99.2%; Pred. No. 3.1e-149;
Matches 496; Conservative 0; Mismatches 0;
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Asselbergs, Fredericus Alphonsus Maria
Hall, Jonathan
Natt, Francois
) OTHER INFORMATION: "Cloning vector pGPlk" US-10-324-493-4
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APPLICANT: Weiler, Jan
APPLICANT: Asselbergs, Fred
APPLICANT: Hall, Jonathan
APPLICANT: Natt, Francois
APPLICANT: Kinzel, Bernd
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SEQ ID NO 5
LENGTH: 4100
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Publication No. US2002018266A1
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: Human Aminoacyl-tRNA Synthetase Polypeptides Useful For TITLE OF INVENTION: The Regulation of Angiogenesis
TITLE OF INVENTION: The Regulation of Angiogenesis
TITLE OF INVENTION: The Regulation of Angiogenesis
CURRENT APPLICATION NUMBER: US/09/813,718
CURRENT PILING DATE: 2001-03-21
NUMBER OF SEQ ID NOS: 58
SOFTWARE: PatentIn Ver. 2.0
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92.4%; Score 462; DB 10;
Best Local Similarity 99.2%; Pred. No. 3.4e-149;
Matches 496; Conservative 0; Mismatches 0;
FILE OF INVENTION: Organic Compounds
FILE REFERENCE: 4-31471
CURRENT APPLICATION NUMBER: US/09/883,573
CURRENT FILING DATE: 2001-06-18
FRIOR PILING DATE: 2000-06-22
PRIOR PILING DATE: 2000-06-22
PRIOR PILING DATE: 2000-06-22
PRIOR FILING DATE: 2000-06-22
PRIOR FILING DATE: 2001-02-07
NUMBER OF SEQ ID NOS: 11
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 1
LENGTH: 4021
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                                                                                                                                                                                                                                                              ; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: plasmid
US-09-883-573-1
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US-09-813-718-5/c
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US-10-240-532-5/c

| Sequence 5, Application US/10240532|
| Sequence 5, Application WS/10240531|
| Subjication No. US2004000916331|
| Publication No. US2004000916331|
| APPLICANT: Schimmel, Paul
| APPLICANT: Wakasugi, Keisuke
| TITLE OF INVENTION: Human Aminoacyl-tRNA Synthetase Polypeptides Useful For TITLE OF INVENTION: The Regulation of Angiogenesis FILE REFERENCE: TSR | 720.1 |
| TITLE OF INVENTION: The Regulation of Angiogenesis FILE REFERENCE: TSR | 720.1 |
| CURRENT APPLICATION NUMBER: US/10/240,532 |
| PRIOR APPLICATION NUMBER: 2001-03-10 |
| PRIOR APPLICATION NUMBER: 2001-03-21 |
| PRIOR APPLICATION NUMBER: 2001-03-31 |
| NUMBER OF SEQ ID NOS: 58 |
| SOFFWARE: PatentIn Ver. 2.0
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                                                                                   FEATURE:

NAME/KEY: CDS

LOCATION: (3428)..(3961)

OTHER INFORMATION: Description of Artificial Sequence:

OTHER INFORMATION: carboxyl-terminal domain in pET20B
US-09-813-718-5
                                                                                                                                                                                                                                                                                           Query Match 92.4%; Score 462; DB 9; Best Local Similarity 99.2%; Pred. No. 3.5e-149; Matches 496; Conservative 0; Mismatches 0;
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LENGTH: 4100
TYPE: DNA
ORGANISM: Artificial Sequence
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1425 GCGAICTGTCTATTTCGTTCAT-CCATAGTTGCCTG--ACTCCCCGTCGTGGAGATAACT 1369
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                                                                                                                                                                                                                                                         4; Gaps
                                                                                                                                human TyrRS
                                                                                                                                                                                                     Query Match 92.4%; Score 462; DB 17; Length 4100; Best Local Similarity 99.2%; Pred. No. 3.5e-149; Matches 496; Conservative 0; Mismatches 0; Indels 4
                                       FEATURE:

NAME/KEY: CDS

LOCATION: (3428)..(3961)

FEATURE:

OTHER INFORMATION: Description of Artificial Sequence:

OTHER INFORMATION: carboxyl-terminal domain in pET20B
US-10-240-532-5
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ORGANISM: Artificial Sequence
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